

SEQUENCE LISTING

<110> Lanahan, Mike

<120> Self-processing Plants and Plant Parts

<130> 109846.317

<140> US 60/315,281

<141> 2001-08-27

<160> 112

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 436

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 1

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Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile
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Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp
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Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val
 65          70          75          80
Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr
      85          90          95
Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His
      100          105          110
Arg Ala Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr
      115          120          125
Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr
      130          135          140
Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe
      145          150          155          160
Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp
      165          170          175
Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly
      180          185          190
Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val
      195          200          205
Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr
      210          215          220
Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly
      225          230          235          240
Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe
      245          250          255
Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly

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Thr	Val	Val	260	Ser	Arg	Asp	Pro	Phe	265	Lys	Ala	Val	Thr	Phe	270	Val	Ala	Asn
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Leu	Thr	Tyr	Glu	Gly	Gln	Pro	Thr	Ile	Phe	Tyr	Arg	Asp	Tyr	Glu	Glu			
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Trp	Leu	Asn	Lys	Asp	Lys	Leu	Lys	Asn	Leu	Ile	Trp	Ile	His	Asp	Asn			
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Leu	Ala	Gly	Gly	Ser	Thr	Ser	Ile	Val	Tyr	Tyr	Asp	Ser	Asp	Glu	Met			
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Ile	Phe	Val	Arg	Asn	Gly	Tyr	Gly	Ser	Lys	Pro	Gly	Leu	Ile	Thr	Tyr			
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Ile	Asn	Leu	Gly	Ser	Ser	Lys	Val	Gly	Arg	Trp	Val	Tyr	Val	Pro	Lys			
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Phe	Ala	Gly	Ala	Cys	Ile	His	Glu	Tyr	Thr	Gly	Asn	Leu	Gly	Gly	Trp			
385				390				395							400			
Val	Asp	Lys	Tyr	Val	Tyr	Ser	Ser	Gly	Trp	Val	Tyr	Leu	Glu	Ala	Pro			
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Ala	Tyr	Asp	Pro	Ala	Asn	Gly	Gln	Tyr	Gly	Tyr	Ser	Val	Trp	Ser	Tyr			
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<211> 1308

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

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<210> 3

<211> 800
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<400> 3

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Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala Lys Asp Val
          35          40          45
Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala Glu Val Trp
          50          55          60
Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro Asp Thr Ser
65          70          75          80
Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val Ile Glu Ala
          85          90          95
Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu Phe Lys Val
          100          105          110
Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu Lys Ala Asp
          115          120          125
Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val Leu Ser Glu
          130          135          140
Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu Ile Ile Glu
145          150          155          160
Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu Asp Asp Tyr
          165          170          175
Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu Lys Thr Ile
          180          185          190
Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val Leu Leu Phe
          195          200          205
Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn Met Glu Tyr
          210          215          220
Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp Leu Asp Gly
225          230          235          240
Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile Arg Thr Thr
          245          250          255
Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln Glu Ser Ala
          260          265          270
Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu Asn Asp Arg
          275          280          285
Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr Glu Ile His
          290          295          300
Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys Asn Lys Gly
305          310          315          320
Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Gly Pro Gly Gly Val
          325          330          335
Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr His Val His
          340          345          350
Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu Asp Lys Asp
          355          360          365
Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu Phe Met Val
          370          375          380
Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His Thr Arg Ile
385          390          395          400

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Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His Gly Ile Gly
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Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile Gly Glu Leu
      420      425      430
Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg Ile Asp Lys
      435      440      445
Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val Ile Ala Ser
      450      455      460
Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val Thr Tyr Trp
      465      470      475      480
Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln Met Gly Leu
      485      490      495
Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu His Lys Ile
      500      505      510
Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly Trp Gly Ala
      515      520      525
Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His Val Ala Ala
      530      535      540
Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val Phe Asn Pro
      545      550      555      560
Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu Thr Lys Ile
      565      570      575
Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys Leu Ile Lys
      580      585      590
Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala Ala Cys His
      595      600      605
Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala Lys Ala Asp
      610      615      620
Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala Gln Lys Leu
      625      630      635      640
Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe Leu His Gly
      645      650      655
Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn Ser Tyr Asn
      660      665      670
Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys Leu Gln Phe
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Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu Arg Lys Glu
      690      695      700
His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys Lys His Leu
      705      710      715      720
Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met Leu Lys Asp
      725      730      735
His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile Tyr Asn Gly
      740      745      750
Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys Trp Asn Val
      755      760      765
Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu Thr Val Glu
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<210> 4
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 <212> DNA
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<223> synthetic

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<210> 5

<211> 693

<212> PRT

<213> *Sulfolobus solfataricus*

<400> 5

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Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile Val Gln Gln
35     40     45
Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys Glu His Ile

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Tyr	Val	Met	Tyr	Asn	Val	Asp	Ala	Gly	Ala	Tyr	Lys	Lys	Tyr	Gln	Asp		
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Pro	Leu	Tyr	Val	Ser	Ile	Pro	Leu	Phe	Ile	Ser	Val	Lys	Asp	Gly	Val		
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Ala	Thr	Gly	Tyr	Phe	Phe	Asn	Ser	Ala	Ser	Lys	Val	Ile	Phe	Asp	Val		
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Val	Glu	Phe	Tyr	Val	Ile	Glu	Gly	Pro	Arg	Ile	Glu	Asp	Val	Leu	Glu		
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Lys	Tyr	Thr	Glu	Leu	Thr	Gly	Lys	Pro	Phe	Leu	Pro	Pro	Met	Trp	Ala		
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Phe	Gly	Tyr	Met	Ile	Ser	Arg	Tyr	Ser	Tyr	Tyr	Pro	Gln	Asp	Lys	Val		
			180					185					190				
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Val	Phe	Leu	Asp	Ile	His	Tyr	Met	Asp	Ser	Tyr	Lys	Leu	Phe	Thr	Trp		
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Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala	Met	Ala	Thr	Phe		
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Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe	Ile	Leu	Ser	Arg		
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Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu	Gln	Leu	Val	Leu		
			420					425					430				
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Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu	Lys	Gly	His	Pro		

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Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu Tyr Ala Pro		
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Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro Arg Gly Lys		
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Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys Ser Val Val		
580	585	590
Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly Ser Ile Ile		
595	600	605
Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr Ser Phe Lys		
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Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu Ile Lys Phe		
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Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser Glu Lys Pro		
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Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln Val Glu Lys		
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Lys Ile Asn Leu Glu		
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<210> 6
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 <212> DNA
 <213> *Sulfolobus solfataricus*

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<211> 1818

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic

<400> 7

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<210> 8

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

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 Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg Thr
 35 40 45
 Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg Gly
 50 55 60
 Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Met Asn Val
 65 70 75 80
 Val Phe Val Gly Ala Glu Met Ala Pro Trp Ser Lys Thr Gly Gly Leu
 85 90 95
 Gly Asp Val Leu Gly Gly Leu Pro Pro Ala Met Ala Ala Asn Gly His
 100 105 110
 Arg Val Met Val Val Ser Pro Arg Tyr Asp Gln Tyr Lys Asp Ala Trp
 115 120 125
 Asp Thr Ser Val Val Ser Glu Ile Lys Met Gly Asp Gly Tyr Glu Thr
 130 135 140
 Val Arg Phe Phe His Cys Tyr Lys Arg Gly Val Asp Arg Val Phe Val
 145 150 155 160
 Asp His Pro Leu Phe Leu Glu Arg Val Trp Gly Lys Thr Glu Glu Lys
 165 170 175
 Ile Tyr Gly Pro Val Ala Gly Thr Asp Tyr Arg Asp Asn Gln Leu Arg
 180 185 190
 Phe Ser Leu Leu Cys Gln Ala Ala Leu Glu Ala Pro Arg Ile Leu Ser
 195 200 205
 Leu Asn Asn Asn Pro Tyr Phe Ser Gly Pro Tyr Gly Glu Asp Val Val
 210 215 220
 Phe Val Cys Asn Asp Trp His Thr Gly Pro Leu Ser Cys Tyr Leu Lys
 225 230 235 240
 Ser Asn Tyr Gln Ser His Gly Ile Tyr Arg Asp Ala Lys Thr Ala Phe
 245 250 255
 Cys Ile His Asn Ile Ser Tyr Gln Gly Arg Phe Ala Phe Ser Asp Tyr
 260 265 270
 Pro Glu Leu Asn Leu Pro Glu Arg Phe Lys Ser Ser Phe Asp Phe Ile
 275 280 285
 Asp Gly Tyr Glu Lys Pro Val Glu Gly Arg Lys Ile Asn Trp Met Lys
 290 295 300
 Ala Gly Ile Leu Glu Ala Asp Arg Val Leu Thr Val Ser Pro Tyr Tyr
 305 310 315 320
 Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg Gly Cys Glu Leu Asp Asn
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 340 345 350
 Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr Ile Ala Val Lys Tyr Asp
 355 360 365
 Val Ser Thr Ala Val Glu Ala Lys Ala Leu Asn Lys Glu Ala Leu Gln
 370 375 380
 Ala Glu Val Gly Leu Pro Val Asp Arg Asn Ile Pro Leu Val Ala Phe
 385 390 395 400
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 405 410 415
 Ile Pro Gln Leu Met Glu Met Val Glu Asp Val Gln Ile Val Leu Leu
 420 425 430
 Gly Thr Gly Lys Lys Lys Phe Glu Arg Met Leu Met Ser Ala Glu Glu
 435 440 445
 Lys Phe Pro Gly Lys Val Arg Ala Val Val Lys Phe Asn Ala Ala Leu

450 455 460
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 485 490 495
 Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu Val Asp Thr Ile Ile Glu
 500 505 510
 Gly Lys Thr Gly Phe His Met Gly Arg Leu Ser Val Asp Cys Asn Val
 515 520 525
 Val Glu Pro Ala Asp Val Lys Lys Val Ala Thr Thr Leu Gln Arg Ala
 530 535 540
 Ile Lys Val Val Gly Thr Pro Ala Tyr Glu Glu Met Val Arg Asn Cys
 545 550 555 560
 Met Ile Gln Asp Leu Ser Trp Lys Gly Pro Ala Lys Asn Trp Glu Asn
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 Val Leu Leu Ser Leu Gly Val Ala Gly Gly Glu Pro Gly Val Glu Gly
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 Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn Val Ala Ala Pro
 595 600 605

<210> 9
 <211> 2223
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

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 gagcagaagg gccccgacgt catggcggcc gccatccgc agctcatgga gatggtggag 1680

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2223

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<210> 10
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 10

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Gln	Lys	Ile	Pro	Glu	Trp	Tyr	Asp	Ala	Gly	Ile	Ser	Ala	Ile	Trp	Ile
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Pro	Pro	Ala	Ser	Lys	Gly	Met	Ser	Gly	Gly	Tyr	Ser	Met	Gly	Tyr	Asp
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Pro	Tyr	Asp	Tyr	Phe	Asp	Leu	Gly	Glu	Tyr	Tyr	Gln	Lys	Gly	Thr	Val
65					70				75					80	
Glu	Thr	Arg	Phe	Gly	Ser	Lys	Gln	Glu	Leu	Ile	Asn	Met	Ile	Asn	Thr
			85					90						95	
Ala	His	Ala	Tyr	Gly	Ile	Lys	Val	Ile	Ala	Asp	Ile	Val	Ile	Asn	His
			100					105					110		
Arg	Ala	Gly	Asp	Leu	Glu	Trp	Asn	Pro	Phe	Val	Gly	Asp	Tyr	Thr	
		115				120					125				
Trp	Thr	Asp	Phe	Ser	Lys	Val	Ala	Ser	Gly	Lys	Tyr	Thr	Ala	Asn	Tyr
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Leu	Asp	Phe	His	Pro	Asn	Glu	Leu	His	Ala	Gly	Asp	Ser	Gly	Thr	Phe
145					150				155					160	
Gly	Gly	Tyr	Pro	Asp	Ile	Cys	His	Asp	Lys	Ser	Trp	Asp	Gln	Tyr	Trp
		165						170					175		
Leu	Trp	Ala	Ser	Gln	Glu	Ser	Tyr	Ala	Ala	Tyr	Leu	Arg	Ser	Ile	Gly
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Ile	Asp	Ala	Trp	Arg	Phe	Asp	Tyr	Val	Lys	Gly	Tyr	Gly	Ala	Trp	Val
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Val	Lys	Asp	Trp	Leu	Asn	Trp	Trp	Gly	Gly	Trp	Ala	Val	Gly	Glu	Tyr
		210				215					220				
Trp	Asp	Thr	Asn	Val	Asp	Ala	Leu	Leu	Asn	Trp	Ala	Tyr	Ser	Ser	Gly
225					230				235					240	
Ala	Lys	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Tyr	Lys	Met	Asp	Ala	Ala	Phe
			245						250				255		
Asp	Asn	Lys	Asn	Ile	Pro	Ala	Leu	Val	Glu	Ala	Leu	Lys	Asn	Gly	Gly
		260						265					270		
Thr	Val	Val	Ser	Arg	Asp	Pro	Phe	Lys	Ala	Val	Thr	Phe	Val	Ala	Asn
		275					280					285			
His	Asp	Thr	Asp	Ile	Ile	Trp	Asn	Lys	Tyr	Pro	Ala	Tyr	Ala	Phe	Ile
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Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu
 305 310 315 320
 Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn
 325 330 335
 Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met
 340 345 350
 Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr
 355 360 365
 Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys
 370 375 380
 Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp
 385 390 395 400
 Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro
 405 410 415
 Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr
 420 425 430
 Cys Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val
 435 440 445
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 465 470 475 480
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 485 490 495
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 545 550 555 560
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 565 570 575
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 580 585 590
 Val Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp
 595 600 605
 Val Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu
 610 615 620
 Gln Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly
 625 630 635 640
 Leu Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg
 645 650 655
 Leu Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val
 660 665 670
 Ala Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr
 675 680 685
 Glu Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly
 690 695 700
 Pro Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly
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 Asn Val Ala Ala Pro
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 <211> 1515
 <212> DNA
 <213> Zea mays

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 <212> DNA
 <213> Zea mays

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 aattgcacgt caagggtatt gggtaagaaa caatcaaaaca aatcctctct gtgtgcaaag 180
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 aacacaagaa attgtgttaa ttaataaaag ctataaataa cgctcgcag cctgtgcact 600
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 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetic

<400> 13

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Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100     105     110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115     120     125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130     135     140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145     150     155     160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165     170     175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180     185     190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195     200     205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210     215     220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225     230     235     240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245     250     255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260     265     270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275     280     285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290     295     300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305     310     315     320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325     330     335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340     345     350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355     360     365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370     375     380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385     390     395     400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
405     410     415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
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Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp

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435
Ser Tyr Cys Gly Val Gly
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440

445

<210> 14
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic

<400> 14

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Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100     105     110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115     120     125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130     135     140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145     150     155     160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165     170     175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180     185     190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195     200     205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210     215     220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225     230     235     240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245     250     255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260     265     270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275     280     285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290     295     300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305     310     315     320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325     330     335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340     345     350

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Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
      355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
      370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385      390      395      400
Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
      405      410      415
Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
      420      425      430
Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
435      440      445
Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
450      455      460

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<210> 15
 <211> 518
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 15
Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
!      5      10      15
Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
      20      25      30
Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35      40      45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50      55      60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65      70      75      80
Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met Gln Ala Phe
      85      90      95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
100      105      110
Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
115      120      125
Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
130      135      140
Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
145      150      155      160
Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
165      170      175
His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
180      185      190
Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
195      200      205
Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
210      215      220
Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
225      230      235      240
Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
245      250      255
Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile

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                260                265                270
Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
                275                280                285
Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
                290                295                300
Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
305                310                315
Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
                325                330                335
Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
                340                345                350
Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
                355                360                365
Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
370                375                380
Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
385                390                395
Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
                405                410                415
Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
                420                425                430
Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
                435                440                445
Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
450                455                460
Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
465                470                475
Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
                485                490                495
Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
500                505                510
Gly Val Gly Thr Ser Ile
515

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<210> 16
 <211> 820
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

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<400> 16
Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
 1                5                10                15
Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
 20                25                30
Leu Arg Gly Ala Arg Ala Ser Ala Ala Asp Thr Leu Ser Met Arg
 35                40                45
Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
 50                55                60
Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
 65                70                75                80
Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met Gln Ala Phe
 85                90                95
Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr Ile Arg Gln
100                105                110

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Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile Trp Ile Pro
 115 120 125
 Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly Tyr Asp Pro
 130 135 140
 Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly Thr Val Glu
 145 150 155 160
 Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile Asn Thr Ala
 165 170 175
 His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile Asn His Arg
 180 185 190
 Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp Tyr Thr Trp
 195 200 205
 Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala Asn Tyr Leu
 210 215 220
 Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly Thr Phe Gly
 225 230 235 240
 Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln Tyr Trp Leu
 245 250 255
 Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser Ile Gly Ile
 260 265 270
 Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala Trp Val Val
 275 280 285
 Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly Glu Tyr Trp
 290 295 300
 Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser Ser Gly Ala
 305 310 315 320
 Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala Ala Phe Asp
 325 330 335
 Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn Gly Gly Thr
 340 345 350
 Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val Ala Asn His
 355 360 365
 Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala Phe Ile Leu
 370 375 380
 Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr Glu Glu Trp
 385 390 395 400
 Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His Asp Asn Leu
 405 410 415
 Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp Glu Met Ile
 420 425 430
 Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile Thr Tyr Ile
 435 440 445
 Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val Pro Lys Phe
 450 455 460
 Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly Gly Trp Val
 465 470 475 480
 Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu Ala Pro Ala
 485 490 495
 Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp Ser Tyr Cys
 500 505 510
 Gly Val Gly Thr Ser Ile Ala Gly Ile Leu Glu Ala Asp Arg Val Leu
 515 520 525
 Thr Val Ser Pro Tyr Tyr Ala Glu Glu Leu Ile Ser Gly Ile Ala Arg
 530 535 540
 Gly Cys Glu Leu Asp Asn Ile Met Arg Leu Thr Gly Ile Thr Gly Ile
 545 550 555 560
 Val Asn Gly Met Asp Val Ser Glu Trp Asp Pro Ser Arg Asp Lys Tyr
 565 570 575

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Ile Ala Val Lys Tyr Asp Val Ser Thr Ala Val Glu Ala Lys Ala Leu
      580      585      590
Asn Lys Glu Ala Leu Gln Ala Glu Val Gly Leu Pro Val Asp Arg Asn
      595      600      605
Ile Pro Leu Val Ala Phe Ile Gly Arg Leu Glu Glu Gln Lys Gly Pro
      610      615      620
Asp Val Met Ala Ala Ala Ile Pro Gln Leu Met Glu Met Val Glu Asp
      625      630      635      640
Val Gln Ile Val Leu Leu Gly Thr Gly Lys Lys Lys Phe Glu Arg Met
      645      650      655
Leu Met Ser Ala Glu Glu Lys Phe Pro Gly Lys Val Arg Ala Val Val
      660      665      670
Lys Phe Asn Ala Ala Leu Ala His His Ile Met Ala Gly Ala Asp Val
      675      680      685
Leu Ala Val Thr Ser Arg Phe Glu Pro Cys Gly Leu Ile Gln Leu Gln
      690      695      700
Gly Met Arg Tyr Gly Thr Pro Cys Ala Cys Ala Ser Thr Gly Gly Leu
      705      710      715      720
Val Asp Thr Ile Ile Glu Gly Lys Thr Gly Phe His Met Gly Arg Leu
      725      730      735
Ser Val Asp Cys Asn Val Val Glu Pro Ala Asp Val Lys Lys Val Ala
      740      745      750
Thr Thr Leu Gln Arg Ala Ile Lys Val Val Gly Thr Pro Ala Tyr Glu
      755      760      765
Glu Met Val Arg Asn Cys Met Ile Gln Asp Leu Ser Trp Lys Gly Pro
      770      775      780
Ala Lys Asn Trp Glu Asn Val Leu Leu Ser Leu Gly Val Ala Gly Gly
      785      790      795      800
Glu Pro Gly Val Glu Gly Glu Glu Ile Ala Pro Leu Ala Lys Glu Asn
      805      810      815
Val Ala Ala Pro
      820

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<210> 17
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 17
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser

<210> 18
 <211> 444
 <212> PRT
 <213> *Thermotoga maritima*

<400> 18
 Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys
 1 5 10 15
 Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val

<210> 19
<211> 1335
<212> DNA

<213> *Thermotoga maritima*

<400> 19

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atggccgagt tcttcccga gatcccgaag atccagttcg agggcaagga gtccaccaac 60
ccgctcgctt tccgcttcta cgaccggaac gaggtgatcg acggcaagcc gctcaaggac 120
caccctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
ggcgaccoga ccgcgagcgc cccgtggaac cgtctctccg acccgatgga caaggccttc 240
gcccgcctgg acgccccttt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
cacgaccgag acatcgcccc ggagggaag accctccgcg agaccaacaa gatcctcgac 360
aagggtggtg agcgcacata ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
accgccaacc tcttctccca cccgcgctac atgcacggcg ccgccaccac ctgctccgcc 480
gacgtgttcg cctacggcgc cgcccagggtg aagaaggccc tggagatcac caaggagctg 540
ggcggcgaag gctacgtgtt ctggggcgac cgagagggtt acgagaccct cctcaacacc 600
gacctcgggc tggagctgga gaacctcgcc cgtctctccc gcatggccgt ggagtacgcc 660
aagaagatcg gcttcaccgg ccagttcttc atcgagccga agccgaagga gccgaccaag 720
caccagtacg acttcgacgt ggccaccgcc tacgccttcc tcaagaacca cggcctcgac 780
gagtaacttca agttcaacat cgaggccaac cacgccacc tcgccggcca cactttccag 840
cacgagctgc gcatggcccgc catcctcggc aagctcggtt ccatcgacgc caaccagggc 900
gacctctctc tcggctggga caccgaccag ttcccgaaca acatctacga caccaccctc 960
gccatgtacg aggtgatcaa ggccggcggc ttaccaaggg gcggcctcaa cttcgacgcc 1020
aagggtcgcc gcgcctccta caagggtggg gacctcttca tcggccacat cgccggcatg 1080
gacaccttcg ccttcggctt caagatcgcc tacaagctcg ccaaggacgg cgtgttcgac 1140
aagttcatcg aggagaagta ccgctccttc aaggagggca tcggcaagga gatcgtggag 1200
ggcaagaccg acttcgagaa gctggaggag tacatcatcg acaaggagga catcgagctg 1260
ccgtccggca agcaggagta cctggagttc ctctcaact cctacatcgt gaagaccatc 1320
gccgagctgc gctga                                     1335

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<210> 20

<211> 444

<212> PRT

<213> *Thermotoga neapolitana*

<400> 20

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Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys
1 5 10 15
Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile
20 25 30
Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe
35 40 45
Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr
50 55 60
Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe
65 70 75 80
Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu
85 90 95
Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu
100 105 110
Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu
115 120 125
Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu
130 135 140
Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala
145 150 155 160
Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile
165 170 175
Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn

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195	200	205
Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly		
210	215	220
Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys		
225	230	235
His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Ser		
245	250	255
His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala		
260	265	270
Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile		
275	280	285
Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu		
290	295	300
Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr Thr Leu		
305	310	315
Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu		
325	330	335
Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu		
340	345	350
Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys		
355	360	365
Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe Ile Glu		
370	375	380
Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile Val Glu		
385	390	395
Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu		
405	410	415
Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Ile		
420	425	430
Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg		
435	440	

<210> 21
 <211> 1335
 <212> DNA
 <213> Thermotoga neapolitana

<400> 21
 atggccgagt tcttcccgga gatcccgaag gtgcagttcg agggcaagga gtccaccaac 60
 ccgctcgcct tcaagttcta cgaccggag gagatcatcg acggcaagcc gctcaaggac 120
 caccctcaagt tctccgtggc cttctggcac accttcgtga acgagggccg cgaccggttc 180
 ggcgaccgga ccgcccagccg cccgtggaac cgctacaccg acccgatgga caaggccttc 240
 gcccgcgtgg acgccctctt cgagttctgc gagaagctca acatcgagta cttctgcttc 300
 cacgaccgag acatcgcccc ggagggcaag accctccgag agaccaacaa gatcctcgac 360
 aagggtgggtg agcgcatcaa ggagcgcatg aaggactcca acgtgaagct cctctggggc 420
 accgccaacc tcttctccca cccgcgctac atgcacggcg ccgcccaccac ctgctccgcc 480
 gacgtgttcg cctacgcccg cgcccaggtg aaagaaggccc tggagatcac caaggagctg 540
 ggcggcgagg gctacgtgtt ctggggcgcc cgcgagggtt acgagaccct cctcaacacc 600
 gacctcggct tcgagctgga gaacctcgcc cgcttcctcc gcatggccgt ggactacgcc 660
 aagcgcatcg gcttcaccgg ccagttcttc atcgagccga agccgaagga gccgaccaag 720
 caccagtagc acttcgacgt ggccaccgcc tacgccttcc tcaagtccca cggcctcgac 780
 gagtacttca agttcaacat cgaggccaac cagccacccc tcgccggcca caccttccag 840
 caccagctgc gcatggcccg catcctcggc aagctcggtt ccatcgacgc caaccagggc 900
 gacctcctcc tcggctggga caccgaccag ttcccgaacca acgtgtacga caccaccttc 960
 gccatgtacg aggtgatcaa ggccggcgcc ttacccaagg gcggcctcaa cttcgacgcc 1020
 aagggtcgcc gcgcctccta caagggtggag gacctcttca tcggccacat cggcgcatg 1080
 gacaccttcg ccctcggtt caaagtggtc tacaagctcg tgaaggacgg cgtgctcgac 1140

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aagttcatcg aggagaagta ccgttccttc cgcgagggca tcggccgcga catcgtggag 1200
ggcaaggttg acttcgagaa gctggaggag tacatcatcg acaaggagac catcgagctg 1260
ccgtccggca agcaggagta cctggagtcc ctcatcaact cctacatcgt gaagaccatc 1320
ctggagctgc gctga                                     1335

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<210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 22
 agcgaattca tggcggtctt ggccacgt 28

<210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 23
 agctaagctt cagggcgagg caacgttct 29

<210> 24
 <211> 825
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 24
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175

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Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
180 185
Asp Asp Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
195 200 205
Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
210 215 220
Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
225 230 235 240
Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
245 250 255
Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
260 265 270
Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
275 280 285
Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
290 295 300
Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr
305 310 315 320
Glu Ile His Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys
325 330 335
Asn Lys Gly Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Ala Pro
340 345 350
Gly Gly Val Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr
355 360 365
His Val His Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu
370 375 380
Asp Lys Asp Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu
385 390 395 400
Phe Met Val Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His
405 410 415
Thr Arg Ile Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His
420 425 430
Gly Ile Gly Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile
435 440 445
Gly Glu Leu Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg
450 455 460
Ile Asp Lys Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val
465 470 475 480
Ile Ala Ser Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val
485 490 495
Thr Tyr Trp Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln
500 505 510
Met Gly Leu Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu
515 520 525
His Lys Ile Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly
530 535 540
Trp Gly Ala Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His
545 550 555 560
Val Ala Ala Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val
565 570 575
Phe Asn Pro Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu
580 585 590
Thr Lys Ile Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys
595 600 605
Leu Ile Lys Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala
610 615 620
Ala Cys His Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala
625 630 635 640

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Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Glu Leu Lys Asn Ala
 645 650 655
 Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
 660 665 670
 Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
 675 680 685
 Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
 690 695 700
 Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
 705 710 715 720
 Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
 725 730 735
 Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
 740 745 750
 Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
 755 760 765
 Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys
 770 775 780
 Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
 785 790 795 800
 Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
 805 810 815
 Tyr Arg Glu Ser Glu Lys Asp Glu Leu
 820 825

<210> 25
 <211> 2478
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 25
 atgagggtgt tgcctcgttc cctcgtcttc ctggctctcg ctgcgagcgc caccagcgct 60
 ggcactggt acaagcacca gcgcgcctac cagttcaccg gcgaggacga cttcgggaag 120
 gtggccgtgg tgaagctccc gatggacctc accaaggtgg gcatcatcgt gcgcctcaac 180
 gagtggcagg cgaaggacgt ggccaaggac cgcttcacgc agatcaagga cggcaaggcc 240
 gaggtgtgga tactccaggg cgtggaggag atcttctacg agaagccgga cacctccccg 300
 cgcattctct tcgcccaggc ccgctccaac aaggtgatcg aggccttcct caccaccccg 360
 gtggacacca agaagaagga gctgttcaag gtgaccgtcg acggcaagga gatcccgggtg 420
 tcccgcgtgg agaaggccga cccgaccgac atcgacgtga ccaactacgt gcgcctcgtg 480
 ctctccgagt ccccaagga ggaggacctc cgcaaggacg tggagctgat catcgagggc 540
 tacaagccgg cccgcgtgat catgatggag atcctcgacg actactacta cgacggcgag 600
 ctgggggcgg tgtactcccc ggagaagacc atcttccgcg tgtgttcccc ggtgtccaag 660
 tgggtgaagg tgcctctctt caagaacggc gaggacaccg agccgtacca ggtggtgaac 720
 atcgagtaca agggcaacgg cgtgtgggag gccgtggtgg agggcgacct cgacggcggtg 780
 ttctacctct accagctgga gaactacggc aagatccgca ccaccgtgga cccgtactcc 840
 aaggccgtgt acgccaacaa ccaggagtct gcagtgggtg acctcgcccg caccaccccg 900
 gagggctggg agaacgaccg cggcccgaag atcgagggtc acgaggacgc catcatctac 960
 gagatccaca tcgccgacat caccggcctg gagaactccg gcgtgaagaa caagggcctc 1020
 tacctcggcc tcaccgagga gaacaccaag gccccgggcg gcgtgaccac cggcctctcc 1080
 caccctcgtg agctgggcgt gacccacgtg cacatcctcc cgttcttcga cttctacacc 1140
 ggcgacgagc tggacaaggga cttcgagaag tactacaact ggggctacga cccgtacctc 1200
 ttcattgtgc cggaggggcg ctactccacc gacccgaaga accgcacac ccgaattcgc 1260
 gaggtgaagg agatgggtga ggccctccac aagcacggca tcggcgtgat catggacatg 1320
 gtgttcccgc acacctacgg catcggcgag ctgtccgcct tcgaccagac cgtgccgtac 1380

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tacttctacc gcatcgacaa gaccggcgcc tacctcaacg agtccggctg cggcaacgtg 1440
atcgccctcc agcgcccgat gatgcgcaag ttcatcgtgg acaccgtgac ctactgggtg 1500
aaggagttacc acatcgacgg cttccgcttc gaccagatgg gcctcatcga caagaagacc 1560
atgctggagg tggagcgcg cctccacaag atcgaccgga ccatcatcct ctacggcgag 1620
ccgtggggcg gctggggggc cccgatccgc ttcggaagt cggacgtggc cggcaccac 1680
gtggccgcct tcaacgacga gttccgcgac gccatccgcg gctccgtgt caaccctgcc 1740
gtgaagggtc tcgtgatggg cggctacggc aaggagacca agatcaagcg cggcgtggtg 1800
ggctccatca actacgacgg caagctcatc aagtccttcg ccctcgaccc ggaggagacc 1860
atcaactacg ccgcctgcca cgacaaccac accctctggg acaagaacta cctcgccgcc 1920
aaggccgaca agaagaagga gtggaccgag gaggagctga agaacgcca gaagctcgcc 1980
ggcgccatcc tcctcactag tcagggcgtg ccgttcctcc acggcgcca ggacttctgc 2040
cgcaccacca acttcaacga caactcctac aacgccccga tctccatcaa cggcttcgac 2100
tacgagcgca agtccagtt catcgacgtg ttcaactacc acaaggcct catcaagctc 2160
cgcaaggagc acccgccctt ccgcctcaag aacgcccagg agatcaagaa gcacctggag 2220
ttctcccg gcgggcgccg catcgtggcc ttcattgctc aggaccacgc cggcgcgac 2280
ccgtggaagg acatcgtggt gatctacaac ggcaacctgg agaagaccac ctacaagctc 2340
ccggagggca agtggaacgt ggtggtgaac tcccagaagg ccggcaccga ggtgatcgag 2400
accgtggagg gcaccatcga gctggacccg ctctccgcct acgtgctcta ccgcgagtc 2460
gagaaggacg agctgtga                                     2478

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<210> 26

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 26

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ser
1          5          10          15
Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
20          25          30
Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
35          40          45
Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
50          55          60
Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
65          70          75          80
Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
85          90          95
Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
100         105         110
Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
115         120         125
Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
130         135         140
Phe Asp Val Gly Leu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
145         150         155         160
Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
165         170         175
Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
180         185         190
Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
195         200         205
Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
210         215         220
Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

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225					230					235				240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile
				245					250					255
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His
			260					265					270	
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly
			275				280				285			
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp
	290					295				300				
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu
305					310					315				320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly
			325						330					335
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu
			340					345					350	
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg
		355					360					365		
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys
	370					375					380			
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala
385					390					395				400
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe
			405						410					415
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile
			420					425					430	
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu
	435						440				445			
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys
	450					455					460			
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser
465					470					475				480
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe
			485						490					495
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe
			500					505					510	
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg
	515						520					525		
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu
	530						535				540			
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp
545					550					555				560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu
			565						570					575
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu
		580						585					590	
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly
	595						600					605		
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu
	610					615					620			
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu
625					630					635				640
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn
			645						650					655
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr
	660							665					670	
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile
	675						680					685		
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln

690 695 700
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 27
 <211> 712
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 27
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
 20 25 30
 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu
 225 230 235 240
 Phe Thr Trp His Pro Tyr Arg Phe Pro Glu Pro Lys Lys Leu Ile Asp
 245 250 255
 Glu Leu His Lys Arg Asn Val Lys Leu Ile Thr Ile Val Asp His Gly
 260 265 270
 Ile Arg Val Asp Gln Asn Tyr Ser Pro Phe Leu Ser Gly Met Gly Lys
 275 280 285
 Phe Cys Glu Ile Glu Ser Gly Glu Leu Phe Val Gly Lys Met Trp Pro
 290 295 300
 Gly Thr Thr Val Tyr Pro Asp Phe Phe Arg Glu Asp Thr Arg Glu Trp
 305 310 315 320
 Trp Ala Gly Leu Ile Ser Glu Trp Leu Ser Gln Gly Val Asp Gly Ile
 325 330 335
 Trp Leu Asp Met Asn Glu Pro Thr Asp Phe Ser Arg Ala Ile Glu Ile
 340 345 350

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Arg Asp Val Leu Ser Ser Leu Pro Val Gln Phe Arg Asp Asp Arg Leu
    355          360          365
Val Thr Thr Phe Pro Asp Asn Val Val His Tyr Leu Arg Gly Lys Arg
    370          375          380
Val Lys His Glu Lys Val Arg Asn Ala Tyr Pro Leu Tyr Glu Ala Met
    385          390          395          400
Ala Thr Phe Lys Gly Phe Arg Thr Ser His Arg Asn Glu Ile Phe Ile
    405          410          415
Leu Ser Arg Ala Gly Tyr Ala Gly Ile Gln Arg Tyr Ala Phe Ile Trp
    420          425          430
Thr Gly Asp Asn Thr Pro Ser Trp Asp Leu Lys Leu Gln Leu Gln
    435          440          445
Leu Val Leu Gly Leu Ser Ile Ser Gly Val Pro Phe Val Gly Cys Asp
    450          455          460
Ile Gly Gly Phe Gln Gly Arg Asn Phe Ala Glu Ile Asp Asn Ser Met
    465          470          475          480
Asp Leu Leu Val Lys Tyr Tyr Ala Leu Ala Leu Phe Phe Pro Phe Tyr
    485          490          495
Arg Ser His Lys Ala Thr Asp Gly Ile Asp Thr Glu Pro Val Phe Leu
    500          505          510
Pro Asp Tyr Tyr Lys Glu Lys Val Lys Glu Ile Val Glu Leu Arg Tyr
    515          520          525
Lys Phe Leu Pro Tyr Ile Tyr Ser Leu Ala Leu Glu Ala Ser Glu Lys
    530          535          540
Gly His Pro Val Ile Arg Pro Leu Phe Tyr Glu Phe Gln Asp Asp Asp
    545          550          555          560
Asp Met Tyr Arg Ile Glu Asp Glu Tyr Met Val Gly Lys Tyr Leu Leu
    565          570          575
Tyr Ala Pro Ile Val Ser Lys Glu Glu Ser Arg Leu Val Thr Leu Pro
    580          585          590
Arg Gly Lys Trp Tyr Asn Tyr Trp Asn Gly Glu Ile Ile Asn Gly Lys
    595          600          605
Ser Val Val Lys Ser Thr His Glu Leu Pro Ile Tyr Leu Arg Glu Gly
    610          615          620
Ser Ile Ile Pro Leu Glu Gly Asp Glu Leu Ile Val Tyr Gly Glu Thr
    625          630          635          640
Ser Phe Lys Arg Tyr Asp Asn Ala Glu Ile Thr Ser Ser Ser Asn Glu
    645          650          655
Ile Lys Phe Ser Arg Glu Ile Tyr Val Ser Lys Leu Thr Ile Thr Ser
    660          665          670
Glu Lys Pro Val Ser Lys Ile Ile Val Asp Asp Ser Lys Glu Ile Gln
    675          680          685
Val Glu Lys Thr Met Gln Asn Thr Tyr Val Ala Lys Ile Asn Gln Lys
    690          695          700
Ile Arg Gly Lys Ile Asn Leu Glu
    705          710

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<210> 28

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 28

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser

1	5	10	15
Ala Thr Ser Met	Ala Glu Phe Phe	Pro Glu Ile Pro Lys	Ile Gln Phe
20	25	30	
Glu Gly Lys Glu	Ser Thr Asn Pro	Leu Ala Phe Arg	Phe Tyr Asp Pro
35	40	45	
Asn Glu Val Ile	Asp Gly Lys Pro	Leu Lys Asp His	Leu Lys Phe Ser
50	55	60	
Val Ala Phe Trp	His Thr Phe Val	Asn Glu Gly Arg	Asp Pro Phe Gly
65	70	75	80
Asp Pro Thr Ala	Glu Arg Pro Trp	Asn Arg Phe Ser	Asp Pro Met Asp
85	90	95	
Lys Ala Phe Ala	Arg Val Asp Ala	Leu Phe Glu Phe	Cys Glu Lys Leu
100	105	110	
Asn Ile Glu Tyr	Phe Cys Phe His	Asp Arg Asp Ile	Ala Pro Glu Gly
115	120	125	
Lys Thr Leu Arg	Glu Thr Asn Lys	Ile Leu Asp Lys	Val Val Glu Arg
130	135	140	
Ile Lys Glu Arg	Met Lys Asp Ser	Asn Val Lys Leu	Leu Trp Gly Thr
145	150	155	160
Ala Asn Leu Phe	Ser His Pro Arg	Tyr Met His Gly	Ala Ala Thr Thr
165	170	175	
Cys Ser Ala Asp	Val Phe Ala Tyr	Ala Ala Ala Gln	Val Lys Lys Ala
180	185	190	
Leu Glu Ile Thr	Lys Glu Leu Gly	Glu Gly Tyr Val	Phe Trp Gly
195	200	205	
Gly Arg Glu Gly	Tyr Glu Thr Leu	Leu Asn Thr Asp	Leu Gly Leu Glu
210	215	220	
Leu Glu Asn Leu	Ala Arg Phe Leu	Arg Met Ala Val	Glu Tyr Ala Lys
225	230	235	240
Lys Ile Gly Phe	Thr Gly Gln Phe	Leu Ile Glu Pro	Lys Pro Lys Glu
245	250	255	
Pro Thr Lys His	Gln Tyr Asp Phe	Asp Val Ala Thr	Ala Tyr Ala Phe
260	265	270	
Leu Lys Asn His	Gly Leu Asp Glu	Tyr Phe Lys Phe	Asn Ile Glu Ala
275	280	285	
Asn His Ala Thr	Leu Ala Gly His	Thr Phe Gln His	Glu Leu Arg Met
290	295	300	
Ala Arg Ile Leu	Gly Lys Leu Gly	Ser Ile Asp Ala	Asn Gln Gly Asp
305	310	315	320
Leu Leu Leu Gly	Trp Asp Thr Asp	Gln Phe Pro Thr	Asn Ile Tyr Asp
325	330	335	
Thr Thr Leu Ala	Met Tyr Glu Val	Ile Lys Ala Gly	Gly Phe Thr Lys
340	345	350	
Gly Gly Leu Asn	Phe Asp Ala Lys	Val Arg Arg Ala	Ser Tyr Lys Val
355	360	365	
Glu Asp Leu Phe	Ile Gly His Ile	Ala Gly Met Asp	Thr Phe Ala Leu
370	375	380	
Gly Phe Lys Ile	Ala Tyr Lys Leu	Ala Lys Asp Gly	Val Phe Asp Lys
385	390	395	400
Phe Ile Glu Glu	Lys Tyr Arg Ser	Phe Lys Glu Gly	Ile Gly Lys Glu
405	410	415	
Ile Val Glu Gly	Lys Thr Asp Phe	Glu Lys Leu Glu	Glu Tyr Ile Ile
420	425	430	
Asp Lys Glu Asp	Ile Glu Leu Pro	Ser Gly Lys Gln	Glu Tyr Leu Glu
435	440	445	
Ser Leu Leu Asn	Ser Tyr Ile Val	Lys Thr Ile Ala	Glu Leu Arg Ser
450	455	460	
Glu Lys Asp Glu	Leu		

465

<210> 29
 <211> 469
 <212> PRT
 <213> Artificial Sequence

<210>
 <223> synthetic

<400> 29
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe
 260 265 270
 Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
 275 280 285
 Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
 290 295 300
 Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
 305 310 315 320
 Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
 325 330 335
 Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
 340 345 350
 Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
 355 360 365

Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
 370 375 380
 Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
 385 390 395 400
 Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
 405 410 415
 Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
 420 425 430
 Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
 435 440 445
 Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg Ser
 450 455 460
 Glu Lys Asp Glu Leu
 465

<210> 30
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 30
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ser
 1 5 10 15
 Ala Thr Ser Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Val Gln Phe
 20 25 30
 Glu Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Lys Phe Tyr Asp Pro
 35 40 45
 Glu Glu Ile Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser
 50 55 60
 Val Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly
 65 70 75 80
 Asp Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp
 85 90 95
 Lys Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu
 100 105 110
 Asn Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly
 115 120 125
 Lys Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg
 130 135 140
 Ile Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr
 145 150 155 160
 Ala Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr
 165 170 175
 Cys Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala
 180 185 190
 Leu Glu Ile Thr Lys Glu Leu Gly Gly Glu Tyr Val Phe Trp Gly
 195 200 205
 Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu
 210 215 220
 Leu Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys
 225 230 235 240
 Arg Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu
 245 250 255
 Pro Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe


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                260                265                270
Leu Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala
                275                280                285
Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met
                290                295                300
Ala Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp
305                310                315                320
Leu Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp
                325                330                335
Thr Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys
                340                345                350
Gly Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val
                355                360                365
Glu Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu
                370                375                380
Gly Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys
385                390                395                400
Phe Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp
                405                410                415
Ile Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile
                420                425                430
Asp Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu
                435                440                445
Ser Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
                450                455                460

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<210> 31
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

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<400> 31
Met Gly Lys Asn Gly Asn Leu Cys Cys Phe Ser Leu Leu Leu Leu Leu
1          5          10          15
Leu Ala Gly Leu Ala Ser Gly His Gln
                20                25

```

<210> 32
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

```

<400> 32
Met Gly Phe Val Leu Phe Ser Gln Leu Pro Ser Phe Leu Leu Val Ser
1          5          10          15
Thr Leu Leu Leu Phe Leu Val Ile Ser His Ser Cys Arg Ala
                20                25                30

```

<210> 33

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 33

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1      5      10      15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Gly Gly Val Ile Met
 20      25      30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
 35      40      45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
 50      55      60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
 65      70      75      80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
 85      90      95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
100      105      110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
115      120      125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
130      135      140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145      150      155      160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
165      170      175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
180      185      190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
195      200      205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
210      215      220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225      230      235      240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
245      250      255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
260      265      270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
275      280      285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
290      295      300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305      310      315      320
Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
325      330      335
Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
340      345      350
Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
355      360      365
Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
370      375      380
Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
385      390      395      400

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Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 34
 <211> 825
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 34
 Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Ala Gly His Trp Tyr Lys His Gln Arg Ala Tyr Gln Phe
 20 25 30
 Thr Gly Glu Asp Asp Phe Gly Lys Val Ala Val Val Lys Leu Pro Met
 35 40 45
 Asp Leu Thr Lys Val Gly Ile Ile Val Arg Leu Asn Glu Trp Gln Ala
 50 55 60
 Lys Asp Val Ala Lys Asp Arg Phe Ile Glu Ile Lys Asp Gly Lys Ala
 65 70 75 80
 Glu Val Trp Ile Leu Gln Gly Val Glu Glu Ile Phe Tyr Glu Lys Pro
 85 90 95
 Asp Thr Ser Pro Arg Ile Phe Phe Ala Gln Ala Arg Ser Asn Lys Val
 100 105 110
 Ile Glu Ala Phe Leu Thr Asn Pro Val Asp Thr Lys Lys Lys Glu Leu
 115 120 125
 Phe Lys Val Thr Val Asp Gly Lys Glu Ile Pro Val Ser Arg Val Glu
 130 135 140
 Lys Ala Asp Pro Thr Asp Ile Asp Val Thr Asn Tyr Val Arg Ile Val
 145 150 155 160
 Leu Ser Glu Ser Leu Lys Glu Glu Asp Leu Arg Lys Asp Val Glu Leu
 165 170 175
 Ile Ile Glu Gly Tyr Lys Pro Ala Arg Val Ile Met Met Glu Ile Leu
 180 185 190
 Asp Asp Tyr Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Ser Pro Glu
 195 200 205
 Lys Thr Ile Phe Arg Val Trp Ser Pro Val Ser Lys Trp Val Lys Val
 210 215 220
 Leu Leu Phe Lys Asn Gly Glu Asp Thr Glu Pro Tyr Gln Val Val Asn
 225 230 235 240
 Met Glu Tyr Lys Gly Asn Gly Val Trp Glu Ala Val Val Glu Gly Asp
 245 250 255
 Leu Asp Gly Val Phe Tyr Leu Tyr Gln Leu Glu Asn Tyr Gly Lys Ile
 260 265 270
 Arg Thr Thr Val Asp Pro Tyr Ser Lys Ala Val Tyr Ala Asn Asn Gln
 275 280 285
 Glu Ser Ala Val Val Asn Leu Ala Arg Thr Asn Pro Glu Gly Trp Glu
 290 295 300
 Asn Asp Arg Gly Pro Lys Ile Glu Gly Tyr Glu Asp Ala Ile Ile Tyr

305 310 315 320
 Glu Ile His Ile Ala Asp Ile Thr Gly Leu Glu Asn Ser Gly Val Lys
 325 330 335
 Asn Lys Gly Leu Tyr Leu Gly Leu Thr Glu Glu Asn Thr Lys Ala Pro
 340 345 350
 Gly Gly Val Thr Thr Gly Leu Ser His Leu Val Glu Leu Gly Val Thr
 355 360 365
 His Val His Ile Leu Pro Phe Phe Asp Phe Tyr Thr Gly Asp Glu Leu
 370 375 380
 Asp Lys Asp Phe Glu Lys Tyr Tyr Asn Trp Gly Tyr Asp Pro Tyr Leu
 385 390 395 400
 Phe Met Val Pro Glu Gly Arg Tyr Ser Thr Asp Pro Lys Asn Pro His
 405 410 415
 Thr Arg Ile Arg Glu Val Lys Glu Met Val Lys Ala Leu His Lys His
 420 425 430
 Gly Ile Gly Val Ile Met Asp Met Val Phe Pro His Thr Tyr Gly Ile
 435 440 445
 Gly Glu Leu Ser Ala Phe Asp Gln Thr Val Pro Tyr Tyr Phe Tyr Arg
 450 455 460
 Ile Asp Lys Thr Gly Ala Tyr Leu Asn Glu Ser Gly Cys Gly Asn Val
 465 470 475 480
 Ile Ala Ser Glu Arg Pro Met Met Arg Lys Phe Ile Val Asp Thr Val
 485 490 495
 Thr Tyr Trp Val Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Gln
 500 505 510
 Met Gly Leu Ile Asp Lys Lys Thr Met Leu Glu Val Glu Arg Ala Leu
 515 520 525
 His Lys Ile Asp Pro Thr Ile Ile Leu Tyr Gly Glu Pro Trp Gly Gly
 530 535 540
 Trp Gly Ala Pro Ile Arg Phe Gly Lys Ser Asp Val Ala Gly Thr His
 545 550 555 560
 Val Ala Ala Phe Asn Asp Glu Phe Arg Asp Ala Ile Arg Gly Ser Val
 565 570 575
 Phe Asn Pro Ser Val Lys Gly Phe Val Met Gly Gly Tyr Gly Lys Glu
 580 585 590
 Thr Lys Ile Lys Arg Gly Val Val Gly Ser Ile Asn Tyr Asp Gly Lys
 595 600 605
 Leu Ile Lys Ser Phe Ala Leu Asp Pro Glu Glu Thr Ile Asn Tyr Ala
 610 615 620
 Ala Cys His Asp Asn His Thr Leu Trp Asp Lys Asn Tyr Leu Ala Ala
 625 630 635 640
 Lys Ala Asp Lys Lys Lys Glu Trp Thr Glu Glu Leu Lys Asn Ala
 645 650 655
 Gln Lys Leu Ala Gly Ala Ile Leu Leu Thr Ser Gln Gly Val Pro Phe
 660 665 670
 Leu His Gly Gly Gln Asp Phe Cys Arg Thr Thr Asn Phe Asn Asp Asn
 675 680 685
 Ser Tyr Asn Ala Pro Ile Ser Ile Asn Gly Phe Asp Tyr Glu Arg Lys
 690 695 700
 Leu Gln Phe Ile Asp Val Phe Asn Tyr His Lys Gly Leu Ile Lys Leu
 705 710 715 720
 Arg Lys Glu His Pro Ala Phe Arg Leu Lys Asn Ala Glu Glu Ile Lys
 725 730 735
 Lys His Leu Glu Phe Leu Pro Gly Gly Arg Arg Ile Val Ala Phe Met
 740 745 750
 Leu Lys Asp His Ala Gly Gly Asp Pro Trp Lys Asp Ile Val Val Ile
 755 760 765
 Tyr Asn Gly Asn Leu Glu Lys Thr Thr Tyr Lys Leu Pro Glu Gly Lys

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      770              775              780
Trp Asn Val Val Val Asn Ser Gln Lys Ala Gly Thr Glu Val Ile Glu
785              790              795              800
Thr Val Glu Gly Thr Ile Glu Leu Asp Pro Leu Ser Ala Tyr Val Leu
      805              810              815
Tyr Arg Glu Ser Glu Lys Asp Glu Leu
      820              825

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<210> 35
 <211> 460
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

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<400> 35
Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1              5              10              15
Ala Thr Ser Ala Lys Tyr Leu Glu Leu Glu Glu Gly Gly Val Ile Met
      20              25              30
Gln Ala Phe Tyr Trp Asp Val Pro Ser Gly Gly Ile Trp Trp Asp Thr
      35              40              45
Ile Arg Gln Lys Ile Pro Glu Trp Tyr Asp Ala Gly Ile Ser Ala Ile
      50              55              60
Trp Ile Pro Pro Ala Ser Lys Gly Met Ser Gly Gly Tyr Ser Met Gly
65              70              75              80
Tyr Asp Pro Tyr Asp Tyr Phe Asp Leu Gly Glu Tyr Tyr Gln Lys Gly
      85              90              95
Thr Val Glu Thr Arg Phe Gly Ser Lys Gln Glu Leu Ile Asn Met Ile
      100              105              110
Asn Thr Ala His Ala Tyr Gly Ile Lys Val Ile Ala Asp Ile Val Ile
      115              120              125
Asn His Arg Ala Gly Gly Asp Leu Glu Trp Asn Pro Phe Val Gly Asp
      130              135              140
Tyr Thr Trp Thr Asp Phe Ser Lys Val Ala Ser Gly Lys Tyr Thr Ala
145              150              155              160
Asn Tyr Leu Asp Phe His Pro Asn Glu Leu His Ala Gly Asp Ser Gly
      165              170              175
Thr Phe Gly Gly Tyr Pro Asp Ile Cys His Asp Lys Ser Trp Asp Gln
      180              185              190
Tyr Trp Leu Trp Ala Ser Gln Glu Ser Tyr Ala Ala Tyr Leu Arg Ser
      195              200              205
Ile Gly Ile Asp Ala Trp Arg Phe Asp Tyr Val Lys Gly Tyr Gly Ala
      210              215              220
Trp Val Val Lys Asp Trp Leu Asn Trp Trp Gly Gly Trp Ala Val Gly
225              230              235              240
Glu Tyr Trp Asp Thr Asn Val Asp Ala Leu Leu Asn Trp Ala Tyr Ser
      245              250              255
Ser Gly Ala Lys Val Phe Asp Phe Pro Leu Tyr Tyr Lys Met Asp Ala
      260              265              270
Ala Phe Asp Asn Lys Asn Ile Pro Ala Leu Val Glu Ala Leu Lys Asn
      275              280              285
Gly Gly Thr Val Val Ser Arg Asp Pro Phe Lys Ala Val Thr Phe Val
      290              295              300
Ala Asn His Asp Thr Asp Ile Ile Trp Asn Lys Tyr Pro Ala Tyr Ala
305              310              315              320

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Phe Ile Leu Thr Tyr Glu Gly Gln Pro Thr Ile Phe Tyr Arg Asp Tyr
 325 330 335
 Glu Glu Trp Leu Asn Lys Asp Lys Leu Lys Asn Leu Ile Trp Ile His
 340 345 350
 Asp Asn Leu Ala Gly Gly Ser Thr Ser Ile Val Tyr Tyr Asp Ser Asp
 355 360 365
 Glu Met Ile Phe Val Arg Asn Gly Tyr Gly Ser Lys Pro Gly Leu Ile
 370 375 380
 Thr Tyr Ile Asn Leu Gly Ser Ser Lys Val Gly Arg Trp Val Tyr Val
 385 390 395 400
 Pro Lys Phe Ala Gly Ala Cys Ile His Glu Tyr Thr Gly Asn Leu Gly
 405 410 415
 Gly Trp Val Asp Lys Tyr Val Tyr Ser Ser Gly Trp Val Tyr Leu Glu
 420 425 430
 Ala Pro Ala Tyr Asp Pro Ala Asn Gly Gln Tyr Gly Tyr Ser Val Trp
 435 440 445
 Ser Tyr Cys Gly Val Gly Ser Glu Lys Asp Glu Leu
 450 455 460

<210> 36

<211> 718

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic

<400> 36

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
 1 5 10 15
 Ala Thr Ser Met Glu Thr Ile Lys Ile Tyr Glu Asn Lys Gly Val Tyr
 20 25 30
 Lys Val Val Ile Gly Glu Pro Phe Pro Pro Ile Glu Phe Pro Leu Glu
 35 40 45
 Gln Lys Ile Ser Ser Asn Lys Ser Leu Ser Glu Leu Gly Leu Thr Ile
 50 55 60
 Val Gln Gln Gly Asn Lys Val Ile Val Glu Lys Ser Leu Asp Leu Lys
 65 70 75 80
 Glu His Ile Ile Gly Leu Gly Glu Lys Ala Phe Glu Leu Asp Arg Lys
 85 90 95
 Arg Lys Arg Tyr Val Met Tyr Asn Val Asp Ala Gly Ala Tyr Lys Lys
 100 105 110
 Tyr Gln Asp Pro Leu Tyr Val Ser Ile Pro Leu Phe Ile Ser Val Lys
 115 120 125
 Asp Gly Val Ala Thr Gly Tyr Phe Phe Asn Ser Ala Ser Lys Val Ile
 130 135 140
 Phe Asp Val Gly Leu Glu Glu Tyr Asp Lys Val Ile Val Thr Ile Pro
 145 150 155 160
 Glu Asp Ser Val Glu Phe Tyr Val Ile Glu Gly Pro Arg Ile Glu Asp
 165 170 175
 Val Leu Glu Lys Tyr Thr Glu Leu Thr Gly Lys Pro Phe Leu Pro Pro
 180 185 190
 Met Trp Ala Phe Gly Tyr Met Ile Ser Arg Tyr Ser Tyr Tyr Pro Gln
 195 200 205
 Asp Lys Val Val Glu Leu Val Asp Ile Met Gln Lys Glu Gly Phe Arg
 210 215 220
 Val Ala Gly Val Phe Leu Asp Ile His Tyr Met Asp Ser Tyr Lys Leu

225					230					235				240
Phe	Thr	Trp	His	Pro	Tyr	Arg	Phe	Pro	Glu	Pro	Lys	Lys	Leu	Ile
				245					250					255
Glu	Leu	His	Lys	Arg	Asn	Val	Lys	Leu	Ile	Thr	Ile	Val	Asp	His
			260					265					270	
Ile	Arg	Val	Asp	Gln	Asn	Tyr	Ser	Pro	Phe	Leu	Ser	Gly	Met	Gly
		275					280				285			Lys
Phe	Cys	Glu	Ile	Glu	Ser	Gly	Glu	Leu	Phe	Val	Gly	Lys	Met	Trp
	290					295				300				Pro
Gly	Thr	Thr	Val	Tyr	Pro	Asp	Phe	Phe	Arg	Glu	Asp	Thr	Arg	Glu
	305				310				315					320
Trp	Ala	Gly	Leu	Ile	Ser	Glu	Trp	Leu	Ser	Gln	Gly	Val	Asp	Gly
			325					330						335
Trp	Leu	Asp	Met	Asn	Glu	Pro	Thr	Asp	Phe	Ser	Arg	Ala	Ile	Glu
		340						345					350	Ile
Arg	Asp	Val	Leu	Ser	Ser	Leu	Pro	Val	Gln	Phe	Arg	Asp	Asp	Arg
	355					360					365			Leu
Val	Thr	Thr	Phe	Pro	Asp	Asn	Val	Val	His	Tyr	Leu	Arg	Gly	Lys
	370				375						380			Arg
Val	Lys	His	Glu	Lys	Val	Arg	Asn	Ala	Tyr	Pro	Leu	Tyr	Glu	Ala
	385			390					395					Met
Ala	Thr	Phe	Lys	Gly	Phe	Arg	Thr	Ser	His	Arg	Asn	Glu	Ile	Phe
			405					410						415
Leu	Ser	Arg	Ala	Gly	Tyr	Ala	Gly	Ile	Gln	Arg	Tyr	Ala	Phe	Ile
		420					425					430		Trp
Thr	Gly	Asp	Asn	Thr	Pro	Ser	Trp	Asp	Asp	Leu	Lys	Leu	Gln	Leu
	435					440				445				Gln
Leu	Val	Leu	Gly	Leu	Ser	Ile	Ser	Gly	Val	Pro	Phe	Val	Gly	Cys
	450				455					460				Asp
Ile	Gly	Gly	Phe	Gln	Gly	Arg	Asn	Phe	Ala	Glu	Ile	Asp	Asn	Ser
	465			470					475					Met
Asp	Leu	Leu	Val	Lys	Tyr	Tyr	Ala	Leu	Ala	Leu	Phe	Phe	Pro	Phe
			485					490					495	Tyr
Arg	Ser	His	Lys	Ala	Thr	Asp	Gly	Ile	Asp	Thr	Glu	Pro	Val	Phe
		500					505						510	Leu
Pro	Asp	Tyr	Tyr	Lys	Glu	Lys	Val	Lys	Glu	Ile	Val	Glu	Leu	Arg
	515					520					525			Tyr
Lys	Phe	Leu	Pro	Tyr	Ile	Tyr	Ser	Leu	Ala	Leu	Glu	Ala	Ser	Glu
	530				535						540			Lys
Gly	His	Pro	Val	Ile	Arg	Pro	Leu	Phe	Tyr	Glu	Phe	Gln	Asp	Asp
	545			550				555						560
Asp	Met	Tyr	Arg	Ile	Glu	Asp	Glu	Tyr	Met	Val	Gly	Lys	Tyr	Leu
			565					570						575
Tyr	Ala	Pro	Ile	Val	Ser	Lys	Glu	Glu	Ser	Arg	Leu	Val	Thr	Leu
	580						585					590		Pro
Arg	Gly	Lys	Trp	Tyr	Asn	Tyr	Trp	Asn	Gly	Glu	Ile	Ile	Asn	Gly
	595				600						605			Lys
Ser	Val	Val	Lys	Ser	Thr	His	Glu	Leu	Pro	Ile	Tyr	Leu	Arg	Glu
	610				615					620				Gly
Ser	Ile	Ile	Pro	Leu	Glu	Gly	Asp	Glu	Leu	Ile	Val	Tyr	Gly	Glu
	625			630				635						Thr
Ser	Phe	Lys	Arg	Tyr	Asp	Asn	Ala	Glu	Ile	Thr	Ser	Ser	Ser	Asn
			645					650						Glu
Ile	Lys	Phe	Ser	Arg	Glu	Ile	Tyr	Val	Ser	Lys	Leu	Thr	Ile	Thr
	660						665					670		Ser
Glu	Lys	Pro	Val	Ser	Lys	Ile	Ile	Val	Asp	Asp	Ser	Lys	Glu	Ile
	675					680					685			Gln
Val	Glu	Lys	Thr	Met	Gln	Asn	Thr	Tyr	Val	Ala	Lys	Ile	Asn	Gln
														Lys

690 695 700
 Ile Arg Gly Lys Ile Asn Leu Glu Ser Glu Lys Asp Glu Leu
 705 710 715

<210> 37
 <211> 1434
 <212> DNA
 <213> *Thermotoga maritima*

<400> 37
 atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
 accctggtgc cagcgqgttc catggccgag ttcttcccgg agatcccga gatccagttc 120
 gagggcaagg agtccaccaa cccgctcgcc ttccgcttct acgacccgaa cgaggtgac 180
 gacggcaagc cgtcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagcgcc gcgaccggtt cggcgaccgg accgcccagc gcccgaggaa ccgcttctcc 300
 gacccgatgg acaaggcctt cgcccgcgtg gacgcccctt tcgagttctg cgagaagctc 360
 aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggagggcaa gaccctccgc 420
 gagaccaaca agatcctcga caagggtgtg gagcgcatca aggagcgcat gaaggactcc 480
 aacgtgaagc tctctgggg caaccgcaac ctcttctccc acccgcgcta catgcacggc 540
 gccgccacca cctgctccgc cgacgtgttc gcctacggcg ccgcccaggt gaagaaggcc 600
 ctggagatca ccaaggagct gggcgggcag ggctacgtgt tctggggcgg ccgcgagggc 660
 tacgagaccc tctcaaacac cgacctcggc ctggagctgg agaacctcgc ccgcttctcc 720
 cgcctggccg tggagtacgc caagaagatc ggcttcaccg gccagttcct catcgagccg 780
 aagccgaagg agccgaccaa gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
 ctcaagaacc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
 ctgcgcggcc acaccttcca gcacgagctg cgcattggccc gcatcctcgg caagctcggc 960
 tccatcgacg ccaaccaggg cgacctcctc ctcggtctgg acaccgacca gttcccggacc 1020
 aacatctacg acaccacctt cgccatgtac gaggtgatca aggccggcgg cttaccaag 1080
 ggcggcctca acttcgacgc caaggtgcgc cgcgcctcct acaaggtgga ggacctcttc 1140
 atcgccacca tcgcccggcat ggacaccttc gccctcggct tcaagatcgc ctacaagctc 1200
 gccaaaggac gcggtgttcga caagttcatc gaggagaagt accgctcctt caaggagggc 1260
 atcggaagg agatcggtga gggcaagacc gacttcgaga agctggagga gtacatcatc 1320
 gacaaggagg acatcgagct gccgtccggc aagcaggagt acctggagtc cctcctcaac 1380
 tcctacatcg tgaagaccat cgccgagctg cgctccgaga aggacgagct gtga 1434

<210> 38
 <211> 477
 <212> PRT
 <213> *Thermotoga maritima*

<400> 38
 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
 1 5 10 15
 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
 20 25 30
 Pro Glu Ile Pro Lys Ile Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
 35 40 45
 Leu Ala Phe Arg Phe Tyr Asp Pro Asn Glu Val Ile Asp Gly Lys Pro
 50 55 60
 Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
 65 70 75 80
 Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Glu Arg Pro Trp
 85 90 95
 Asn Arg Phe Ser Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
 100 105 110
 Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
 115 120 125

Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
 130 135 140
 Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
 145 150 155 160
 Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
 165 170 175
 Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
 180 185 190
 Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
 195 200 205
 Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
 210 215 220
 Leu Asn Thr Asp Leu Gly Leu Glu Leu Glu Asn Leu Ala Arg Phe Leu
 225 230 235 240
 Arg Met Ala Val Glu Tyr Ala Lys Lys Ile Gly Phe Thr Gly Gln Phe
 245 250 255
 Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe
 260 265 270
 Asp Val Ala Thr Ala Tyr Ala Phe Leu Lys Asn His Gly Leu Asp Glu
 275 280 285
 Tyr Phe Lys Phe Asn Ile Glu Ala Asn His Ala Thr Leu Ala Gly His
 290 295 300
 Thr Phe Gln His Glu Leu Arg Met Ala Arg Ile Leu Gly Lys Leu Gly
 305 310 315 320
 Ser Ile Asp Ala Asn Gln Gly Asp Leu Leu Leu Gly Trp Asp Thr Asp
 325 330 335
 Gln Phe Pro Thr Asn Ile Tyr Asp Thr Thr Leu Ala Met Tyr Glu Val
 340 345 350
 Ile Lys Ala Gly Gly Phe Thr Lys Gly Gly Leu Asn Phe Asp Ala Lys
 355 360 365
 Val Arg Arg Ala Ser Tyr Lys Val Glu Asp Leu Phe Ile Gly His Ile
 370 375 380
 Ala Gly Met Asp Thr Phe Ala Leu Gly Phe Lys Ile Ala Tyr Lys Leu
 385 390 395 400
 Ala Lys Asp Gly Val Phe Asp Lys Phe Ile Glu Glu Lys Tyr Arg Ser
 405 410 415
 Phe Lys Glu Gly Ile Gly Lys Glu Ile Val Glu Gly Lys Thr Asp Phe
 420 425 430
 Glu Lys Leu Glu Glu Tyr Ile Ile Asp Lys Glu Asp Ile Glu Leu Pro
 435 440 445
 Ser Gly Lys Gln Glu Tyr Leu Glu Ser Leu Leu Asn Ser Tyr Ile Val
 450 455 460
 Lys Thr Ile Ala Glu Leu Arg Ser Glu Lys Asp Glu Leu
 465 470 475

<210> 39
 <211> 1434
 <212> DNA
 <213> Thermotoga neapolitana

<400> 39
 atgaaagaaa ccgctgctgc taaattcgaa cgccagcaca tggacagccc agatctgggt 60
 accctgggtc cagcggttc catggccgag ttcttcccgg agatcccgaa ggtgcagttc 120
 gagggcaagg agtccaccaa cccgctcgcc ttcaagttct acgaccggga ggagatcatc 180
 gacggcaagc cgtcaagga ccacctcaag ttctccgtgg ccttctggca caccttcgtg 240
 aacgagggcc gcgaccggtt cggcgacccg accgcccacc gcccgaggaa ccgctacacc 300
 gacccgatgg acaaggcctt cgcccgcgtg gacgccctct tcgagttctg cgagaagctc 360

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aacatcgagt acttctgctt ccacgaccgc gacatcgccc cggaggggcaa gaccctccgc 420
gagaccaaca agatcctcga caaggtgggt gagcgcatca aggagcgcat gaaggactcc 480
aacgtgaagc tctctgagg caccgccaac ctcttctccc acccgcgta catgcacggc 540
gcccgcacca cctgctccgc cgacgtgttc gcctacgccc ccgcccaggt gaagaaggcc 600
ctggagatca ccaaggagct gggcggcgag ggctacgtgt tctggggcgg ccgcgagggc 660
tacgagaccc tctcaaacac cgacctcggc ttcgagctgg agaacctcgc ccgcttcttc 720
cgcatggcgg tggactacgc caagcgcatc ggcttcaccg gccagtctct catcgagccg 780
aagccgaagg agccgacca gcaccagtac gacttcgacg tggccaccgc ctacgccttc 840
ctcaagtccc acggcctcga cgagtacttc aagttcaaca tcgaggccaa ccacgccacc 900
ctcgccggcc acaccttcca gcacgagctg cgcctggccc gcctcctcgg caagctcggc 960
tccatcgacg ccaaccaggg cgacctcttc ctggctggg acaccgacca gttcccgacc 1020
aacgtgtacg acaccacct cggcatgtac gaggtgatca aggcggcggg cttaccaag 1080
ggcgccctca acttcgacgc caagtgccgc cgcgcctcct acaaggtgga ggacctcttc 1140
atcgccaca tcgccggcat ggacaccttc gccctcggct tcaaggtggc ctacaagctc 1200
gtgaaggacg gcgtgctcga caagttcatc gaggagaagt accgctcctt ccgcgagggc 1260
atcgcccgcg acatcgtgga ggcaagggtg gacttcgaga agctggagga gtacatcatc 1320
gacaaggaga ccatcgagct gccgtccggc aagcaggagt acctggagtc cctcatcaac 1380
tctacatcg tgaagaccat cctggagctg cgctccgaga aggacgagct gtga 1434

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<210> 40

<211> 477

<212> PRT

<213> Thermotoga neapolitana

<400> 40

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Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser
1          5          10          15
Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Met Ala Glu Phe Phe
20          25          30
Pro Glu Ile Pro Lys Val Gln Phe Glu Gly Lys Glu Ser Thr Asn Pro
35          40          45
Leu Ala Phe Lys Phe Tyr Asp Pro Glu Glu Ile Ile Asp Gly Lys Pro
50          55          60
Leu Lys Asp His Leu Lys Phe Ser Val Ala Phe Trp His Thr Phe Val
65          70          75          80
Asn Glu Gly Arg Asp Pro Phe Gly Asp Pro Thr Ala Asp Arg Pro Trp
85          90          95
Asn Arg Tyr Thr Asp Pro Met Asp Lys Ala Phe Ala Arg Val Asp Ala
100          105          110
Leu Phe Glu Phe Cys Glu Lys Leu Asn Ile Glu Tyr Phe Cys Phe His
115          120          125
Asp Arg Asp Ile Ala Pro Glu Gly Lys Thr Leu Arg Glu Thr Asn Lys
130          135          140
Ile Leu Asp Lys Val Val Glu Arg Ile Lys Glu Arg Met Lys Asp Ser
145          150          155          160
Asn Val Lys Leu Leu Trp Gly Thr Ala Asn Leu Phe Ser His Pro Arg
165          170          175
Tyr Met His Gly Ala Ala Thr Thr Cys Ser Ala Asp Val Phe Ala Tyr
180          185          190
Ala Ala Ala Gln Val Lys Lys Ala Leu Glu Ile Thr Lys Glu Leu Gly
195          200          205
Gly Glu Gly Tyr Val Phe Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu
210          215          220
Leu Asn Thr Asp Leu Gly Phe Glu Leu Glu Asn Leu Ala Arg Phe Leu
225          230          235          240
Arg Met Ala Val Asp Tyr Ala Lys Arg Ile Gly Phe Thr Gly Gln Phe
245          250          255
Leu Ile Glu Pro Lys Pro Lys Glu Pro Thr Lys His Gln Tyr Asp Phe

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[illegible]

cctggagctcc ctccctcaact cctacatcgt gaagaccatc gccgagctgc gctga 1435

<210> 42
 <211> 473
 <212> PRT
 <213> Thermotoga maritima

<400> 42
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
 20 25 30
 Ile Pro Met Ala Glu Phe Phe Pro Glu Ile Pro Lys Ile Gln Phe Glu
 35 40 45
 Gly Lys Glu Ser Thr Asn Pro Leu Ala Phe Arg Phe Tyr Asp Pro Asn
 50 55 60
 Glu Val Ile Asp Gly Lys Pro Leu Lys Asp His Leu Lys Phe Ser Val
 65 70 75 80
 Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
 85 90 95
 Pro Thr Ala Glu Arg Pro Trp Asn Arg Phe Ser Asp Pro Met Asp Lys
 100 105 110
 Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
 115 120 125
 Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
 130 135 140
 Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
 145 150 155 160
 Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
 165 170 175
 Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
 180 185 190
 Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
 195 200 205
 Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
 210 215 220
 Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Leu Glu Leu
 225 230 235 240
 Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Glu Tyr Ala Lys Lys
 245 250 255
 Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
 260 265 270
 Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
 275 280 285
 Lys Asn His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
 290 295 300
 His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
 305 310 315 320
 Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
 325 330 335
 Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Ile Tyr Asp Thr
 340 345 350
 Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
 355 360 365
 Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu
 370 375 380
 Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
 385 390 395 400

<400> 44																
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
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Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	
			20					25					30			
Ile	Pro	Met	Ala	Glu	Phe	Phe	Pro	Glu	Ile	Pro	Lys	Val	Gln	Phe	Glu	
		35					40					45				
Gly	Lys	Glu	Ser	Thr	Asn	Pro	Leu	Ala	Phe	Lys	Phe	Tyr	Asp	Pro	Glu	
	50					55					60					
Glu	Ile	Ile	Asp	Gly	Lys	Pro	Leu	Lys	Asp	His	Leu	Lys	Phe	Ser	Val	

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65      70      75      80
Ala Phe Trp His Thr Phe Val Asn Glu Gly Arg Asp Pro Phe Gly Asp
      85      90      95
Pro Thr Ala Asp Arg Pro Trp Asn Arg Tyr Thr Asp Pro Met Asp Lys
      100      105      110
Ala Phe Ala Arg Val Asp Ala Leu Phe Glu Phe Cys Glu Lys Leu Asn
      115      120      125
Ile Glu Tyr Phe Cys Phe His Asp Arg Asp Ile Ala Pro Glu Gly Lys
      130      135      140
Thr Leu Arg Glu Thr Asn Lys Ile Leu Asp Lys Val Val Glu Arg Ile
      145      150      155
Lys Glu Arg Met Lys Asp Ser Asn Val Lys Leu Leu Trp Gly Thr Ala
      160      165      170      175
Asn Leu Phe Ser His Pro Arg Tyr Met His Gly Ala Ala Thr Thr Cys
      180      185      190
Ser Ala Asp Val Phe Ala Tyr Ala Ala Ala Gln Val Lys Lys Ala Leu
      195      200      205
Glu Ile Thr Lys Glu Leu Gly Gly Glu Gly Tyr Val Phe Trp Gly Gly
      210      215      220
Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asp Leu Gly Phe Glu Leu
      225      230      235
Glu Asn Leu Ala Arg Phe Leu Arg Met Ala Val Asp Tyr Ala Lys Arg
      240      245      250      255
Ile Gly Phe Thr Gly Gln Phe Leu Ile Glu Pro Lys Pro Lys Glu Pro
      260      265      270
Thr Lys His Gln Tyr Asp Phe Asp Val Ala Thr Ala Tyr Ala Phe Leu
      275      280      285
Lys Ser His Gly Leu Asp Glu Tyr Phe Lys Phe Asn Ile Glu Ala Asn
      290      295      300
His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu Leu Arg Met Ala
      305      310      315
Arg Ile Leu Gly Lys Leu Gly Ser Ile Asp Ala Asn Gln Gly Asp Leu
      320      325      330      335
Leu Leu Gly Trp Asp Thr Asp Gln Phe Pro Thr Asn Val Tyr Asp Thr
      340      345      350
Thr Leu Ala Met Tyr Glu Val Ile Lys Ala Gly Gly Phe Thr Lys Gly
      355      360      365
Gly Leu Asn Phe Asp Ala Lys Val Arg Arg Ala Ser Tyr Lys Val Glu
      370      375      380
Asp Leu Phe Ile Gly His Ile Ala Gly Met Asp Thr Phe Ala Leu Gly
      385      390      395      400
Phe Lys Val Ala Tyr Lys Leu Val Lys Asp Gly Val Leu Asp Lys Phe
      405      410      415
Ile Glu Glu Lys Tyr Arg Ser Phe Arg Glu Gly Ile Gly Arg Asp Ile
      420      425      430
Val Glu Gly Lys Val Asp Phe Glu Lys Leu Glu Glu Tyr Ile Ile Asp
      435      440      445
Lys Glu Thr Ile Glu Leu Pro Ser Gly Lys Gln Glu Tyr Leu Glu Ser
      450      455      460
Leu Ile Asn Ser Tyr Ile Val Lys Thr Ile Leu Glu Leu Arg
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<210> 45
<211> 1095
<212> PRT
<213> Aspergillus shirousami

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 20 25 30
 Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
 35 40 45
 Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
 50 55 60
 Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
 65 70 75 80
 Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
 85 90 95
 Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
 100 105 110
 Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
 115 120 125
 Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
 130 135 140
 Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
 145 150 155 160
 Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
 165 170 175
 Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
 180 185 190
 Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
 195 200 205
 Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
 210 215 220
 Val Tyr Cys Ile Gly Glu Val Leu Asp Val Asp Pro Ala Tyr Thr Cys
 225 230 235 240
 Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
 245 250 255
 Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
 260 265 270
 Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
 275 280 285
 Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300
 Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320
 Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
 325 330 335
 Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350
 Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
 355 360 365
 Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
 370 375 380
 Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400
 Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
 405 410 415
 Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
 420 425 430
 Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
 435 440 445
 Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr

450	455	460
Pro Thr Glu Lys Leu	Ala Gly Ser Lys Ile Cys	Ser Ser Ser Lys Pro
465	470	475
Ala Thr Leu Asp Ser	Trp Leu Ser Asn Glu Ala Thr	Val Ala Arg Thr
	485	490
Ala Ile Leu Asn Asn	Ile Gly Ala Asp Gly Ala Trp	Val Ser Gly Ala
	500	505
Asp Ser Gly Ile Val	Val Ala Ser Pro Ser Thr	Asp Asn Pro Asp Tyr
	515	520
Phe Tyr Thr Trp Thr	Arg Asp Ser Gly Ile Val	Leu Lys Thr Leu Val
	530	535
Asp Leu Phe Arg Asn	Gly Asp Thr Asp Leu Leu	Ser Thr Ile Glu His
545	550	555
Tyr Ile Ser Ser Gln	Ala Ile Ile Gln Gly Val	Ser Asn Pro Ser Gly
	565	570
Asp Leu Ser Ser Gly	Gly Leu Gly Glu Pro Lys	Phe Asn Val Asp Glu
	580	585
Thr Ala Tyr Ala Gly	Ser Trp Gly Arg Pro Gln	Arg Asp Gly Pro Ala
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Leu Arg Ala Thr Ala	Met Ile Gly Phe Gly Gln	Trp Leu Leu Asp Asn
	610	615
Gly Tyr Thr Ser Ala	Ala Thr Glu Ile Val Trp	Pro Leu Val Arg Asn
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Asp Leu Ser Tyr Val	Ala Gln Tyr Trp Asn Gln	Thr Gly Tyr Asp Leu
	645	650
Trp Glu Glu Val Asn	Gly Ser Ser Phe Phe Thr	Ile Ala Val Gln His
	660	665
Arg Ala Leu Val Glu	Gly Ser Ala Phe Ala Thr	Ala Val Gly Ser Ser
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Cys Ser Trp Cys Asp	Ser Gln Ala Pro Gln Ile	Leu Cys Tyr Leu Gln
	695	700
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705	710	715
Ser Gly Lys Asp Thr	Asn Thr Leu Leu Gly	Ser Ile His Thr Phe Asp
	725	730
Pro Glu Ala Gly Cys	Asp Asp Ser Thr Phe Gln	Pro Cys Ser Pro Arg
	740	745
Ala Leu Ala Asn His	Lys Glu Val Val Asp	Ser Phe Arg Ser Ile Tyr
	755	760
Thr Leu Asn Asp Gly	Leu Ser Asp Ser Glu Ala	Val Ala Val Gly Arg
	770	775
Tyr Pro Glu Asp Ser	Tyr Tyr Asn Gly Asn Pro	Trp Phe Leu Cys Thr
785	790	795
Leu Ala Ala Ala Glu	Gln Leu Tyr Asp Ala Leu	Tyr Gln Trp Asp Lys
	805	810
Gln Gly Ser Leu Glu	Ile Thr Asp Val Ser Leu	Asp Phe Phe Lys Ala
	820	825
Leu Tyr Ser Gly Ala	Ala Thr Gly Thr Tyr Ser	Ser Ser Ser Ser Thr
	835	840
Tyr Ser Ser Ile Val	Ser Ala Val Lys Thr Phe	Ala Asp Gly Phe Val
	850	855
Ser Ile Val Glu Thr	His Ala Ala Ser Asn	Gly Ser Leu Ser Glu Gln
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Phe Asp Lys Ser Asp	Gly Asp Glu Leu Ser Ala	Arg Asp Leu Thr Trp
	885	890
Ser Tyr Ala Ala Leu	Leu Thr Ala Asn Asn	Arg Arg Asn Ser Val Val
	900	905
Pro Pro Ser Trp Gly	Glu Thr Ser Ala Ser	Ser Val Pro Gly Thr Cys

Ala	Ala	Thr	Ser	Ala	Ser	Gly	Thr	Tyr	Ser	Ser	Val	Thr	Val	Thr	Ser
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Trp	Pro	Ser	Ile	Val	Ala	Thr	Gly	Gly	Thr	Thr	Thr	Thr	Ala	Thr	Thr
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Thr	Gly	Ser	Gly	Gly	Val	Thr	Ser	Thr	Ser	Lys	Thr	Thr	Thr	Thr	Ala
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Ser	Lys	Thr	Ser	Thr	Thr	Thr	Ser	Ser	Thr	Ser	Cys	Thr	Thr	Pro	Thr
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			995				1000						1005		
Asn	Ile	Tyr	Leu	Val	Gly	Ser	Ile	Ser	Gln	Leu	Gly	Asp	Trp	Glu	Thr
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Ser	Asp	Gly	Ile	Ala	Leu	Ser	Ala	Asp	Lys	Tyr	Thr	Ser	Ser	Asn	Pro
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Pro	Trp	Tyr	Val	Thr	Val	Thr	Leu	Pro	Ala	Gly	Glu	Ser	Phe	Glu	Tyr
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Lys	Phe	Ile	Arg	Val	Glu	Ser	Asp	Asp	Ser	Val	Glu	Trp	Glu	Ser	Asp
			1060					1065					1070		
Pro	Asn	Arg	Glu	Tyr	Thr	Val	Pro	Gln	Ala	Cys	Gly	Glu	Ser	Thr	Ala
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Thr	Val	Thr	Asp	Thr	Trp	Arg									
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<210> 46

<211> 3285

<212> DNA

<213> *Aspergillus shirousami*

<400> 46

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acctggcagg gcatcatcga caagctcgac tacatccagg gcatgggctt caccgccatc 180
tgatcacc cggtagccgc ccagctcccg cagaccaccg cctacggcga cgcctaccac 240
ggctactggc agcaggacat ctactccctc aacgagaact acggcaccgc cgacgacctc 300
aaggccctct cctccgccct ccacgagcgc ggcatgtacc tcatgggtga cgtgggtggc 360
aaccacatgg gctacgacgg cgccggctcc tccgtggact actccgtgtt caagccgttc 420
tctccacagg actacttcca ccggttctgc ttcatccaga actacgagga ccagaccag 480
gtggaggact gctggctcgg cgacaacacc gtgtccctcc cggacctcga caccaccaag 540
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gacggcctcc gcatcgacac cgtgaagcac gtgcagaagg acttctggcc gggctacaac 660
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gccttcaagt ccacctccgg ctcgatggac gacctctaca acatgatcaa caccgtgaag 840
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ctcatcgct ccgccaacgc catccgcaac tacgccatc ccaaggacac cggcttcgtg 1140
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<210> 47

<211> 679

<212> PRT

<213> Thermoanaerobacterium thermosaccharolyticum

<400> 47

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Phe Asn Asn Ile Ser Ala Val Asn Gly Pro Gly Glu Glu Asp Thr Trp
20     25     30
Ala Ser Ala Gln Lys Gln Gly Val Gly Thr Ala Asn Asn Tyr Val Ser
35     40     45
Arg Val Trp Phe Thr Leu Ala Asn Gly Ala Ile Ser Glu Val Tyr Tyr
50     55     60
Pro Thr Ile Asp Thr Ala Asp Val Lys Glu Ile Lys Phe Ile Val Thr
65     70     75     80
Asp Gly Lys Ser Phe Val Ser Asp Glu Thr Lys Asp Ala Ile Ser Lys
85     90     95
Val Glu Lys Phe Thr Asp Lys Ser Leu Gly Tyr Lys Leu Val Asn Thr
100    105    110
Asp Lys Lys Gly Arg Tyr Arg Ile Thr Lys Glu Ile Phe Thr Asp Val
115    120    125
Lys Arg Asn Ser Leu Ile Met Lys Ala Lys Phe Glu Ala Leu Glu Gly
130    135    140
Ser Ile His Asp Tyr Lys Leu Tyr Leu Ala Tyr Asp Pro His Ile Lys
145    150    155    160
Asn Gln Gly Ser Tyr Asn Glu Gly Tyr Val Ile Lys Ala Asn Asn Asn
165    170    175
Glu Met Leu Met Ala Lys Arg Asp Asn Val Tyr Thr Ala Leu Ser Ser

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Page 51

1	5	10	15
Asp Gly Ser Thr Phe Ser Gly Lys Ile Tyr Val Lys Asn Ile Ala Tyr			
	20	25	30
Ser Lys Lys Val Thr Val Ile Tyr Ala Asp Gly Ser Asp Asn Trp Asn			
	35	40	45
Asn Asn Gly Asn Thr Ile Ala Ala Ser Tyr Ser Ala Pro Ile Ser Gly			
	50	55	60
Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys			
	65	70	75
Glu Phe Tyr Ile Lys Tyr Glu Val Ser Gly Lys Thr Tyr Tyr Asp Asn			
	85	90	95
Asn Asn Ser Ala Asn Tyr Gln Val Ser Thr Ser Lys Pro Thr Thr Thr			
	100	105	110
Thr Ala Thr Ala Thr Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Thr			
	115	120	125
Pro Pro Ser Arg Ser Glu Pro Ala Thr Phe Pro Thr Gly Asn Ser Thr			
	130	135	140
Ile Ser Ser Trp Ile Lys Lys Gln Glu Gly Ile Ser Arg Phe Ala Met			
	145	150	155
Leu Arg Asn Ile Asn Pro Pro Gly Ser Ala Thr Gly Phe Ile Ala Ala			
	165	170	175
Ser Leu Ser Thr Ala Gly Pro Asp Tyr Tyr Tyr Ala Trp Thr Arg Asp			
	180	185	190
Ala Ala Leu Thr Ser Asn Val Ile Val Tyr Glu Tyr Asn Thr Thr Leu			
	195	200	205
Ser Gly Asn Lys Thr Ile Leu Asn Val Leu Lys Asp Tyr Val Thr Phe			
	210	215	220
Ser Val Lys Thr Gln Ser Thr Ser Thr Val Cys Asn Cys Leu Gly Glu			
	225	230	235
Pro Lys Phe Asn Pro Asp Ala Ser Gly Tyr Thr Gly Ala Trp Gly Arg			
	245	250	255
Pro Gln Asn Asp Gly Pro Ala Glu Arg Ala Thr Thr Phe Ile Leu Phe			
	260	265	270
Ala Asp Ser Tyr Leu Thr Gln Thr Lys Asp Ala Ser Tyr Val Thr Gly			
	275	280	285
Thr Leu Lys Pro Ala Ile Phe Lys Asp Leu Asp Tyr Val Val Asn Val			
	290	295	300
Trp Ser Asn Gly Cys Phe Asp Leu Trp Glu Glu Val Asn Gly Val His			
	305	310	315
Phe Tyr Thr Leu Met Val Met Arg Lys Gly Leu Leu Leu Gly Ala Asp			
	325	330	335
Phe Ala Lys Arg Asn Gly Asp Ser Thr Arg Ala Ser Thr Tyr Ser Ser			
	340	345	350
Thr Ala Ser Thr Ile Ala Asn Lys Ile Ser Ser Phe Trp Val Ser Ser			
	355	360	365
Asn Asn Trp Ile Gln Val Ser Gln Ser Val Thr Gly Gly Val Ser Lys			
	370	375	380
Lys Gly Leu Asp Val Ser Thr Leu Leu Ala Ala Asn Leu Gly Ser Val			
	385	390	395
Asp Asp Gly Phe Phe Thr Pro Gly Ser Glu Lys Ile Leu Ala Thr Ala			
	405	410	415
Val Ala Val Glu Asp Ser Phe Ala Ser Leu Tyr Pro Ile Asn Lys Asn			
	420	425	430
Leu Pro Ser Tyr Leu Gly Asn Ser Ile Gly Arg Tyr Pro Glu Asp Thr			
	435	440	445
Tyr Asn Gly Asn Gly Asn Ser Gln Gly Asn Ser Trp Phe Leu Ala Val			
	450	455	460
Thr Gly Tyr Ala Glu Leu Tyr Tyr Arg Ala Ile Lys Glu Trp Ile Gly			

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<210> 51
<211> 439
<212> PRT
<213> Artificial Sequence
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<220>

<223> synthetic

<400> 51

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 20      25      30
Gln Gly Phe Asn Trp Glu Ser Trp Lys Lys Gln Gly Gly Trp Tyr Asn
 35      40      45
Tyr Leu Leu Gly Arg Val Asp Asp Ile Ala Ala Thr Gly Ala Thr His
 50      55      60
Val Trp Leu Pro Gln Pro Ser His Ser Val Ala Pro Gln Gly Tyr Met
 65      70      75      80
Pro Gly Arg Leu Tyr Asp Leu Asp Ala Ser Lys Tyr Gly Thr His Ala
 85      90      95
Glu Leu Lys Ser Leu Thr Ala Ala Phe His Ala Lys Gly Val Gln Cys
100      105      110
Val Ala Asp Val Val Ile Asn His Arg Cys Ala Asp Tyr Lys Asp Gly
115      120      125
Arg Gly Ile Tyr Cys Val Phe Glu Gly Gly Thr Pro Asp Ser Arg Leu
130      135      140
Asp Trp Gly Pro Asp Met Ile Cys Ser Asp Asp Thr Gln Tyr Ser Asn
145      150      155      160
Gly Arg Gly His Arg Asp Thr Gly Ala Asp Phe Ala Ala Ala Pro Asp
165      170      175
Ile Asp His Leu Asn Pro Arg Val Gln Gln Glu Leu Ser Asp Trp Leu
180      185      190
Asn Trp Leu Lys Ser Asp Leu Gly Phe Asp Gly Trp Arg Leu Asp Phe
195      200      205
Ala Lys Gly Tyr Ser Ala Ala Val Ala Lys Val Tyr Val Asp Ser Thr
210      215      220
Ala Pro Thr Phe Val Val Ala Glu Ile Trp Ser Ser Leu His Tyr Asp
225      230      235      240
Gly Asn Gly Glu Pro Ser Ser Asn Gln Asp Ala Asp Arg Gln Glu Leu
245      250      255
Val Asn Trp Ala Gln Ala Val Gly Gly Pro Ala Ala Ala Phe Asp Phe
260      265      270
Thr Thr Lys Gly Val Leu Gln Ala Ala Val Gln Gly Glu Leu Trp Arg
275      280      285
Met Lys Asp Gly Asn Gly Lys Ala Pro Gly Met Ile Gly Trp Leu Pro
290      295      300
Glu Lys Ala Val Thr Phe Val Asp Asn His Asp Thr Gly Ser Thr Gln
305      310      315      320
Asn Ser Trp Pro Phe Pro Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr
325      330      335
Ile Leu Thr His Pro Gly Thr Pro Cys Ile Phe Tyr Asp His Val Phe
340      345      350
Asp Trp Asn Leu Lys Gln Glu Ile Ser Ala Leu Ser Ala Val Arg Ser
355      360      365
Arg Asn Gly Ile His Pro Gly Ser Glu Leu Asn Ile Leu Ala Ala Asp
370      375      380
Gly Asp Leu Tyr Val Ala Lys Ile Asp Asp Lys Val Ile Val Lys Ile
385      390      395      400
Gly Ser Arg Tyr Asp Val Gly Asn Leu Ile Pro Ser Asp Phe His Ala
405      410      415
Val Ala His Gly Asn Asn Tyr Cys Val Trp Glu Lys His Gly Leu Arg
420      425      430

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Val Pro Ala Gly Arg His His
435

<210> 52
<211> 1320
<212> DNA
<213> Artificial Sequence

<220> .
<223> synthetic

<400> 52
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aagaagcaag gtgggtggta caactacctc ctggggcggg tggacgacat cggcgcgacg 180
ggggccacgc acgtctggct cccgcagccg tcgcactcgg tggcgccgca ggggtacatg 240
cccggccggc tctacgacct ggacgcgtcc aagtacggca cccacgcgga gctcaagtgc 300
ctcaccgcgg cgttccacgc caagggcgtc cagtgcgtcg ccgacgtcgt gatcaaccac 360
cgctgcgcgg actacaagga cggccgcggc atctactgcg tcttcgaggg cggcacgccc 420
gacagccggc tcgactgggg ccccacatg atctgcagcg acgacacgca gtactccaac 480
gggcgcgggc accgcgacac gggggccgac ttcgcgcggc cgcccacat cgaccacctc 540
aaccgcgcgg tgcagcagga gctctcggac tggctcaact ggctcaagtc cgacctcggc 600
ttcgacggct ggcgccctcg cttcgccaag ggctactccg ccgcccgtcg caaggtgtac 660
gtcgacagca ccgccccac cttcgtcgtc gccgagatat ggagctccct cactacgac 720
ggcaacggcg agccgtccag caaccaggac gccgacaggc aggagctggt caactgggcg 780
caggcggtgg cgggccccgc cgcggcggtc gacttcacca ccaagggcgt gctgcaggcg 840
gcggtccagg gcgagctgtg gcgcatgaag gacggcaacg gcaaggcgcc cgggatgac 900
ggctggctgc cggagaaggc cgtcacgttc gtcgacaacc acgacaccgg ctccacgcag 960
aactcgtggc catccccctc cgacaaggte atgcagggct acgectatat cctcacgcac 1020
ccagggaactc catgcattct ctacgaccac gttttcgact ggaacctgaa gcaggagatc 1080
agcgcgctgt ctgcggtgag gtcaagaaac gggatccacc cggggagcga gctgaacatc 1140
ctcgcgcgcg acggggatct ctacgtcgcc aagattgacg acaaggtcat cgtgaagatc 1200
gggtcacggt acgacgtcgg gaacctgac cctcagact tccacgccgt tgcccctggc 1260
aacaactact gcgtttggga gaagcacggt ctgagagttc cagcggggcg gcaccactag 1320

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220> .
<223> synthetic

<400> 53
Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Thr Thr Gly Ser Gly Gly
1 5 10 15
Val Thr Ser Thr Ser Lys Thr Thr Thr Thr Ala Ser Lys Thr Ser Thr
20 25 30
Thr Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr Ala Val
35 40 45

<210> 54
<211> 137
<212> DNA
<213> Artificial Sequence

<220>

<223> synthetic

<400> 54

gccaccggcg gcaccaccac caccgccacc accaccggct ccggcggcgt gacctccacc 60
 tccaagacca ccaccaccgc ctccaagacc tccaccacca cctctccac ctctgcacc 120
 accccgaccg ccgtgtc 137

<210> 55

<211> 300

<212> PRT

<213> *Pyrococcus furiosus*

<400> 55

Ile	Tyr	Phe	Val	Glu	Lys	Tyr	His	Thr	Ser	Glu	Asp	Lys	Ser	Thr	Ser
1				5					10				15		
Asn	Thr	Ser	Ser	Thr	Pro	Pro	Gln	Thr	Thr	Leu	Ser	Thr	Thr	Lys	Val
			20					25					30		
Leu	Lys	Ile	Arg	Tyr	Pro	Asp	Asp	Gly	Glu	Trp	Pro	Gly	Ala	Pro	Ile
		35					40					45			
Asp	Lys	Asp	Gly	Asp	Gly	Asn	Pro	Glu	Phe	Tyr	Ile	Glu	Ile	Asn	Leu
	50					55					60				
Trp	Asn	Ile	Leu	Asn	Ala	Thr	Gly	Phe	Ala	Glu	Met	Thr	Tyr	Asn	Leu
65				70					75						80
Thr	Ser	Gly	Val	Leu	His	Tyr	Val	Gln	Gln	Leu	Asp	Asn	Ile	Val	Leu
			85					90						95	
Arg	Asp	Arg	Ser	Asn	Trp	Val	His	Gly	Tyr	Pro	Glu	Ile	Phe	Tyr	Gly
			100					105					110		
Asn	Lys	Pro	Trp	Asn	Ala	Asn	Tyr	Ala	Thr	Asp	Gly	Pro	Ile	Pro	Leu
		115					120				125				
Pro	Ser	Lys	Val	Ser	Asn	Leu	Thr	Asp	Phe	Tyr	Leu	Thr	Ile	Ser	Tyr
		130				135					140				
Lys	Leu	Glu	Pro	Lys	Asn	Gly	Leu	Pro	Ile	Asn	Phe	Ala	Ile	Glu	Ser
145					150					155					160
Trp	Leu	Thr	Arg	Glu	Ala	Trp	Arg	Thr	Thr	Gly	Ile	Asn	Ser	Asp	Glu
			165					170						175	
Gln	Glu	Val	Met	Ile	Trp	Ile	Tyr	Tyr	Asp	Gly	Leu	Gln	Pro	Ala	Gly
		180						185					190		
Ser	Lys	Val	Lys	Glu	Ile	Val	Val	Pro	Ile	Ile	Val	Asn	Gly	Thr	Pro
		195					200					205			
Val	Asn	Ala	Thr	Phe	Glu	Val	Trp	Lys	Ala	Asn	Ile	Gly	Trp	Glu	Tyr
		210				215					220				
Val	Ala	Phe	Arg	Ile	Lys	Thr	Pro	Ile	Lys	Glu	Gly	Thr	Val	Thr	Ile
225					230					235					240
Pro	Tyr	Gly	Ala	Phe	Ile	Ser	Val	Ala	Ala	Asn	Ile	Ser	Ser	Leu	Pro
			245						250					255	
Asn	Tyr	Thr	Glu	Leu	Tyr	Leu	Glu	Asp	Val	Glu	Ile	Gly	Thr	Glu	Phe
			260					265					270		
Gly	Thr	Pro	Ser	Thr	Thr	Ser	Ala	His	Leu	Glu	Trp	Trp	Ile	Thr	Asn
		275					280					285			
Ile	Thr	Leu	Thr	Pro	Leu	Asp	Arg	Pro	Leu	Ile	Ser				
		290				295					300				

<210> 56

<211> 903

<212> DNA

<213> *Pyrococcus furiosus*

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<400> 56
atctacttcg tggagaagta ccacacctcc gaggacaagt ccacctccaa cacctcctcc 60
accccgccgc agaccaccct ctccaccacc aagggtgctca agatccgcta cccggacgac 120
ggcgagtggc ccggcgcccc gatcgacaag gacggcgacg gcaaccggga gttctacatc 180
gagatcaacc tctggaacat cctcaacgcc accggcttcg ccgagatgac ctacaacctc 240
actagtggcg tgcctccacta cgtgcagcag ctcgacaaca tcgtgctccg cgaccgctcc 300
aactgggtgc acggctaccc ggaaatcttc tacggcaaca agccgtggaa cgccaactac 360
gccaccgacg qcccgatccc gctcccgtcc aagggtgtcca acctcaccga cttctacctc 420
accatctcct acaagctcga gccgaagaac ggtctcccga tcaacttcgc catcgagtcc 480
tggctcaccg gcgaggcctg gcgcaccacc ggcatacaact ccgacgagca ggaggtgatg 540
atctggatct actacgacgg cctccagccc gcgggctcca aggtgaagga gatcgtggtg 600
ccgatcatcg tgaacggcac ccggtgaac gccaccttcg aggtgtggaa ggccaacatc 660
ggctgggagt acgtggcctt ccgcatcaag accccgatca aggagggcac cgtgaccatc 720
ccgtacggcg ccttcattctc cgtggccgcc aacatctcct ccctcccgaa ctacaccgag 780
aagtacctcg aggcgtgga gatcggcacc gatttcggca ccccgccac cacctccgcc 840
cacttcgagt ggtggatcac caacatcacc ctacccccgc tcgaccgccc gctcatctcc 900
tag 903

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<210> 57
<211> 387
<212> PRT
<213> Thermus flavus

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<400> 57
Met Tyr Glu Pro Lys Pro Glu His Arg Phe Thr Phe Gly Leu Trp Thr
1 5 10 15
Val Asp Asn Val Asp Arg Asp Pro Phe Gly Asp Thr Val Arg Glu Arg
20 25 30
Leu Asp Pro Val Tyr Val Val His Lys Leu Ala Glu Leu Gly Ala Tyr
35 40 45
Gly Val Asn Leu His Asp Glu Asp Leu Ile Pro Arg Gly Thr Pro Pro
50 55 60
Gln Glu Arg Asp Gln Ile Val Arg Arg Phe Lys Lys Ala Leu Asp Glu
65 70 75 80
Thr Val Leu Lys Val Pro Met Val Thr Ala Asn Leu Phe Ser Glu Pro
85 90 95
Ala Phe Arg Asp Gly Ala Ser Thr Thr Arg Asp Pro Trp Val Trp Ala
100 105 110
Tyr Ala Leu Arg Lys Ser Leu Glu Thr Met Asp Leu Gly Ala Glu Leu
115 120 125
Gly Ala Glu Ile Tyr Met Phe Trp Met Val Arg Glu Arg Ser Glu Val
130 135 140
Glu Ser Thr Asp Lys Thr Arg Lys Val Trp Asp Trp Val Arg Glu Thr
145 150 155 160
Leu Asn Phe Met Thr Ala Tyr Thr Glu Asp Gln Gly Tyr Gly Tyr Arg
165 170 175
Phe Ser Val Glu Pro Lys Pro Asn Glu Pro Arg Gly Asp Ile Tyr Phe
180 185 190
Thr Thr Val Gly Ser Met Leu Ala Leu Ile His Thr Leu Asp Arg Pro
195 200 205
Glu Arg Phe Gly Leu Asn Pro Glu Phe Ala His Glu Thr Met Ala Gly
210 215 220
Leu Asn Phe Asp His Ala Val Ala Gln Ala Val Asp Ala Gly Lys Leu
225 230 235 240
Phe His Ile Asp Leu Asn Asp Gln Arg Met Ser Arg Phe Asp Gln Asp
245 250 255
Leu Arg Phe Gly Ser Glu Asn Leu Lys Ala Gly Phe Phe Leu Val Asp
260 265 270

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Leu Leu Glu Ser Ser Gly Tyr Gln Gly Pro Arg His Phe Glu Ala His
 275 280 285
 Ala Leu Arg Thr Glu Asp Glu Glu Gly Val Trp Thr Phe Val Arg Val
 290 295 300
 Cys Met Arg Thr Tyr Leu Ile Ile Lys Val Arg Ala Glu Thr Phe Arg
 305 310 315 320
 Glu Asp Pro Glu Val Lys Glu Leu Leu Ala Ala Tyr Tyr Gln Glu Asp
 325 330 335
 Pro Ala Thr Leu Ala Leu Leu Asp Pro Tyr Ser Arg Glu Lys Ala Glu
 340 345 350
 Ala Leu Lys Arg Ala Glu Leu Pro Leu Glu Thr Lys Arg Arg Arg Gly
 355 360 365
 Tyr Ala Leu Glu Arg Leu Asp Gln Leu Ala Val Glu Tyr Leu Leu Gly
 370 375 380
 Val Arg Gly
 385

<210> 58
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 58
 atggggaaga acggcaacct gtgctgcttc tctctgctgc tgcttcttct cgccgggttg 60
 qcgctccggcc atcaaatcta cttcgtggag aagtaccaca cctccgagga caagtccacc 120
 tccaacacct cctccacccc gccgcagacc accctctcca ccaccaagggt gctcaagatc 180
 cgctaccggg acgacgggtga gtggcccggc gccccgatcg acaaggacgg cgacggcaac 240
 ccggagtctt acatcgagat caacctctgg aacatcctca acgccaccgg cttcgccgag 300
 atgacctaca acctcaactg tggcgtgctc cactacgtgc agcagctcga caacatcggt 360
 ctccggcagcc gctccaactg ggtgcacggc taccgggaaa tcttctacgg caacaaggcg 420
 tggaaacgcca actacgccac cgacggcccg atcccgctcc cgtccaagggt gtccaacctc 480
 accgacttct acctcaccat ctctacaag ctcgagccga agaacggtct cccgatcaac 540
 ttcgccatcg agtcttggt caccgcgag gccctggcgca ccaccggcat caactccgac 600
 gaggcaggag tgatgatctg gatctactac gacggcctcc agcccgcggg ctccaagggt 660
 aaggagatcg tgggtgccgat catcgtgaac ggcaccccg tgaacgccac cttcgagggt 720
 tggaaaggcca acatcggtg ggaagtacgt gccctccgca tcaagacccc gatcaaggag 780
 ggcaccgtga ccattccgta cggcgcttc atctccgtgg ccgccaacat ctctccctc 840
 ccgaactaca ccgagaagta cctcgaggac gtggagatcg gcaccgagtt cggcaccg 900
 tccaccacct ccgcccacct cgagtgggtg atcaccaaca tcacctcac cccgctcgac 960
 cgcccgctca tctcctag 978

<210> 59
 <211> 1920
 <212> DNA
 <213> *Aspergillus niger*

<400> 59
 atgtccttcc gctccctcct cgcctctccc ggctcgtgt gcaccggcct cgccaacgtg 60
 atctccaagc ggcaccacct cgactcctgg ctctccaac aggccaccgt ggcccgcacc 120
 gccatcctca acaacatcgg cgccgacggc gcctgggtgt ccggcgccga ctccggcatc 180
 gtgggtggcct ccccgctccac cgacaacccg gactacttct acacctggac ccgcgactcc 240
 ggctcgtgc tcaagacctc cgtggacctc ttccgcaac gcgacacctc cctcctctcc 300
 accatcgaga actacatctc cgcccaggcc atcgtgcagg gcatctccaa cccgtccggc 360
 gacctctcct ccggcgccgg cctcggcgag ccgaagttca acgtggacga gaccgcctac 420

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accggctcct ggggcccgcc gcagcgcgac ggccccggccc tccgcgccac cgccatgac 480
ggcttcggcc agtggctcct cgacaacggc tacacctcca ccgccaccga catcgtgtgg 540
ccgctcgtgc gcaacgacct ctcttacgtg gccagtagt ggaaccagac cggctacgac 600
ctctgggagg aggtgaacgg ctctccttc ttcacatcg ccgtgcagca ccgcgcctc 660
gtggagggct ccgccttcgc caccgcggtg ggctcctcct gctcctgggt cgaactccag 720
gccccggaga tctctgtcta cctccagtc ttctggaccg gctccttcac cctcgccaac 780
ttcgactcct ccgctccgg caaggacgcc aacacctcc tcggctccat ccacaccttc 840
gacccggagg ccgctcgcga cgactccacc ttccagccgt gctccccgg cgccctcgcc 900
aaccacaagg aggtggtgga ctcttcgc tcctctaca cctcaacga cggcctctcc 960
gactccgagg ccgtggccgt ggcccgctac ccggaggaca cctactaaa cggcaaccgg 1020
tggttcctct gcacctcgc cgcgcgcgag cagctctacg acgacctcta ccagtgggac 1080
aagcagggct cctcgaagg gaccgacgtg tccctcgact tcttcaaggc cctctactcc 1140
gacgcgcgca ccggcaccta ctctcctcc tctccacct actcctccat cgtggacgcc 1200
gtgaagacct tcgcccgcgg ctctcgtgct atcgtggaga cccacgcgc ctccaacggc 1260
tccatgtccg agcagtagca caagtccgac ggcgagcagc tctccgccc cgaacctacc 1320
tggtcctacg ccgacctcct caccgccaac aaccgcgcga actccgtgg gccggcctcc 1380
tggggcgaga cctccgcctc ctccgtgccc ggcacctgcg ccgccacct cgcctatggc 1440
acctactcct ccgtgacctg gacctcctgg ccgtccatcg tggccaccgg cggcaccacc 1500
accaccgcca ccccgaccgg ctccggctcc gtgacctcca cctccaagac caccgccacc 1560
gcctccaaga cctccacctc cactcctcc acctcctgca ccacctcgac cgcgtggcc 1620
gtgaccttcg acctcaccgc caccaccacc tacggcgaga acatctacct cgtgggctcc 1680
atctcccagc tgggcgactg ggagacctcc gacggcatcg cctctccgc cgacaagtac 1740
acctcctccg acccgctctg gtacgtgacc gtgacctcc cggccggcga gtccttcgag 1800
tacaagttca tccgcatcga gtccgacgac tccgtggagt gggagtccga cccgaaccgc 1860
gagtagaccg tccgcgaggc ctgcggcacc tccaccgcca ccgtgaccga cactggcgcc 1920

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<210> 60
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<400> 60
 Ser Glu Lys Asp Glu Leu
 1 5

<210> 61
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD7436

<220>
 <221> CDS
 <222> (1)..(561)

<400> 61
 atg gct agc acc ttc tac tgg cat ttg tgg acc gac ggc atc ggc acc 48
 Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
 1 5 10 15

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gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc      96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
      20                      25                      30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct      144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
      35                      40                      45

acc agg gtg atc aac tac aac gct cat gct ttc agc gtg gtg ggc aac      192
Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
      50                      55                      60

gct tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac      240
Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
      65                      70                      75                      80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag      288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
      85                      90                      95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc      336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
      100                      105                      110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa      384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
      115                      120                      125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc      432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
      130                      135                      140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac      480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
      145                      150                      155                      160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa      528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
      165                      170                      175

agc agc ggc tac agc aac gtg acc gtg tgg tag      561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
      180                      185

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<210> 62
<211> 186
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 62

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Met Ala Ser Thr Phe Tyr Trp His Leu Trp Thr Asp Gly Ile Gly Thr
1      5      10      15

```

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45
 Thr Arg Val Ile Asn Tyr Asn Ala His Ala Phe Ser Val Val Gly Asn
 50 55 60
 Ala Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 63
 <211> 561
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Xylanase BD6002A

<220>
 <221> CDS
 <222> (1)..(561)

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<400> 63
atg gct agc acc gac tac tgg caa aac tgg acc gac ggc ggc ggc acc 48
Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
i 5 10 15

gtg aac gct acc aac ggc agc gac ggc aac tac agc gtg agc tgg agc 96
Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc agc gct 144
Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
35 40 45

acc agg gtg atc aac tac aac gct ggc gct ttc agc cca agc ggc aac 192
Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
50 55 60

ggc tac ttg gct ttg tac ggc tgg acc agg aac agc ttg atc gag tac 240
Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
65 70 75 80

tac gtg gtg gac agc tgg ggc acc tac agg cca acc ggc acc tac aag 288
Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
85 90 95

ggc acc gtg acc agc gac ggc ggc acc tac gac atc tac acc acc acc 336
Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
100 105 110

agg acc aac gct cca agc atc gac ggc aac aac acc acc ttc acc caa 384
Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
115 120 125

ttc tgg agc gtg agg caa agc aag agg cca atc ggc acc aac aac acc 432
Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
130 135 140

atc acc ttc agc aac cat gtg aac gct tgg aag agc aag ggc atg aac 480
Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
145 150 155 160

ttg ggc agc agc tgg agc tac caa gtg ttg gct acc gag ggc tac caa 528
Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
165 170 175

agc agc ggc tac agc aac gtg acc gtg tgg tag 561
Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
180 185

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<210> 64
<211> 186
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 64

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 65

<211> 561

<212> DNA

<213> Artificial Sequence

<220>

<223> Xylanase BD6002B

<220>

<221> CDS

<222> (1) .. (561)

<400> 65

atg gcc tcc acc gac tac tgg cag aac tgg acc gac ggc ggc ggc acc 48
 Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

gtg aac gcc acc aac ggc tcc gac ggc aac tac tcc gtg tcc tgg tcc 96
 Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

aac tgc ggc aac ttc gtg gtg ggc aag ggc tgg acc acc ggc tcc gcc 144
 Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

acc cgc gtg atc aac tac aac gcc ggc gcc ttc tcc ccg tcc ggc aac 192
 Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

ggc tac ctc gcc ctc tac ggc tgg acc cgc aac tcc ctc atc gag tac 240
 Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

tac gtg gtg gac tcc tgg ggc acc tac cgc ccg acc ggc acc tac aag 288
 Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

ggc acc gtg acc tcc gac ggc ggc acc tac gac atc tac acc acc acc 336
 Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

cgc acc aac gcc ccg tcc atc gac ggc aac aac acc acc ttc acc cag 384
 Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

ttc tgg tcc gtg cgc cag tcc aag cgc ccg atc ggc acc aac aac acc 432
 Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

atc acc ttc tcc aac cac gtg aac gcc tgg aag tcc aag ggc atg aac 480
 Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

ctc ggc tcc tcc tgg tcc tac cag gtg ctc gcc acc gag ggc tac cag 528
 Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

tcc tcc ggc tac tcc aac gtg acc gtg tgg tga 561
 Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 66

<211> 186

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 66

Met Ala Ser Thr Asp Tyr Trp Gln Asn Trp Thr Asp Gly Gly Gly Thr
 1 5 10 15

Val Asn Ala Thr Asn Gly Ser Asp Gly Asn Tyr Ser Val Ser Trp Ser
 20 25 30

Asn Cys Gly Asn Phe Val Val Gly Lys Gly Trp Thr Thr Gly Ser Ala
 35 40 45

Thr Arg Val Ile Asn Tyr Asn Ala Gly Ala Phe Ser Pro Ser Gly Asn
 50 55 60

Gly Tyr Leu Ala Leu Tyr Gly Trp Thr Arg Asn Ser Leu Ile Glu Tyr
 65 70 75 80

Tyr Val Val Asp Ser Trp Gly Thr Tyr Arg Pro Thr Gly Thr Tyr Lys
 85 90 95

Gly Thr Val Thr Ser Asp Gly Gly Thr Tyr Asp Ile Tyr Thr Thr Thr
 100 105 110

Arg Thr Asn Ala Pro Ser Ile Asp Gly Asn Asn Thr Thr Phe Thr Gln
 115 120 125

Phe Trp Ser Val Arg Gln Ser Lys Arg Pro Ile Gly Thr Asn Asn Thr
 130 135 140

Ile Thr Phe Ser Asn His Val Asn Ala Trp Lys Ser Lys Gly Met Asn
 145 150 155 160

Leu Gly Ser Ser Trp Ser Tyr Gln Val Leu Ala Thr Glu Gly Tyr Gln
 165 170 175

Ser Ser Gly Tyr Ser Asn Val Thr Val Trp
 180 185

<210> 67
 <211> 2071

<212> DNA
 <213> *Oryza sativa*

<220>
 <221> misc_feature
 <222> (1)..(2071)
 <223> Promoter

<400> 67
 tccatgctgt cctactactt gcttcacccc ctctacatt ttgttctggt ttttggcctg 60
 catcttcggat catgatgtat gtgatttcca atctgctgca atatgaatgg agactctgtg 120
 ctaaccatca acaacatgaa atgcttatga ggcctttgct gagcagccaa tcttgccctgt 180
 gtttaigtct tcacaggccg aattcctctg ttttgtttt caccctcaat atttggaaac 240
 atttatctag gtgtttgtg tccaggccta taaatcatac atgatgttgt cgtattggat 300
 gtgaatgtgg tggcgtgttc agtgccctgg atttgagttt gatgagagtt gcttctgggt 360
 caccactcac cattatcgat gctcctcttc agcataaggt aaaagtcttc cctgtttacg 420
 ttattttacc cactatgggt gcttgggttg gtttttctt gattgcttat gccatggaaa 480
 gtcatttgat atgttgaact tgaattact gtagaattgt atacatgttc catttgtgtt 540
 gtacttcctt cttttctatt agtagcctca gatgagtgtg aaaaaaacag attatataac 600
 ttgccctata aatcatttga aaaaaatatt gtacagtgaag aaattgatat atagtgaatt 660
 ttttaagagca tgttttctta aagaagtata tattttctat gtacaaaggc cattgaagta 720
 attgtagata caggataatg tagacttttt ggacttacac tgctaccttt aagtaacaat 780
 catgagcaat agtgttgcaa tgatatttag gctgcattcg ttactctct tgatttccat 840
 gagcacgctt cccaaactgt taaactctgt gttttttgcc aaaaaaaaaat gcataggaaa 900
 gttgctttta aaaaatcata tcaatccatt ttttaagtta tagctaatac ttaattaatc 960
 atgcgctaatt aagtcactct gtttttcgta cttagagagat tgttttgaac cagcactcaa 1020
 gaacacagcc ttaaccagc caaataatgc tacaacctac cagtccacac ctcttgtaaa 1080
 gcatttggtg catggaaaag ctaagatgac agcaacctgt tcaggaaaac aactgacaag 1140
 gtcataggga gagggagctt ttggaaaagg gccgtgcagt tcaaacaatt agtttagcagt 1200
 aggggtgttg tttttgctca cagcaataag aagttaatca tgggtgtaggc aacccaaata 1260
 aaacacccaaa atatgcacaa ggcagtttgt tgtattctgt agtacagaca aaactaaaag 1320
 taatgaaaga agatgtggtg ttagaaaagg aaacaatatc atgagtaatg tgtgggcatt 1380
 atgggaccac gaaataaaaa gaacattttg atgagtcgtg tctctcgat gagcctcaaa 1440

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agttctctca ccccgataa gaaaccctta agcaatgtgc aaagtttgca ttctccactg 1500
acataatgca aaataagata tcacgatga catagcaact catgcatcat atcatgcctc 1560
ttccaacctt ttcatctcta ctcatctaca taagtatctt cagctaaatg ttagaacata 1620
aaccataaag tcacgtttga tgagtattag gcgtgacaca tgacaaatca cagactcaag 1680
caagataaag caaaatgatg tgtacataaa actccagagc tatatgtcat attgcaaaaa 1740
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agaggagggc ttacatttat ccattgtcata ttgcaaaaga aagagagaaa gaacaacaca 1860
atgctgcgtc aattatacat atctgtatgt ccattcattat tcattccact ttcgtgtacc 1920
acatttcata tatcatgagt cacttcattg ctggacatta acaaaactta tcttaacatt 1980
tagatgcaag agcctttatc tcaactataaa tgcacgatga ttcttcattg ttcttcacaa 2040
aaagcattca gttcattagt cctacaacaa c 2071

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<210> 68
<211> 79
<212> PRT
<213> Zea mays

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<220>
<221> SIGNAL
<222> (1)..(79)
<223> Maize waxy signal sequence.

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<400> 68

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Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1          5          10          15

```

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Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
20          25          30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
35          40          45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
50          55          60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala
65          70          75

```

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<210> 69
<211> 1005

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<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Synthetic Bromelain Sequence

<220>
 <221> CDS
 <222> (1)..(1005)
 <223> Synthetic Bromelain

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<400> 69
atg gcc tgg aag gtg cag gtg gtg ttc ctc ttc ctc ttc ctc tgc gtg      48
Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
1          5          10          15

atg tgg gcc tcc ccg tcc gcc gcc tcc gcg gac gag ccg tcc gac ccg      96
Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
          20          25          30

atg atg aag cgc ttc gag gag tgg atg gtg gag tac ggc cgc gtg tac      144
Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
          35          40          45

aag gac aac gac gag aag atg cgc cgc ttc cag atc ttc aag aac aac      192
Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
          50          55          60

gtg aac cac atc gag acc ttc aac tcc cgc aac gag aac tcc tac acc      240
Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
65          70          75          80

ctc ggc atc aac cag ttc acc gac atg acc aac aac gag ttc atc gcc      288
Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
          85          90          95

cag tac acc ggc ggc atc tcc cgc ccg ctc aac atc gag cgc gag ccg      336
Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
          100          105          110

gtg gtg tcc ttc gac gac gtg gac atc tcc gcc gtg ccg cag tcc atc      384
Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
          115          120          125

gac tgg cgc gac tac ggc gcc gtg acc tcc gtg aag aac cag aac ccg      432
Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
          130          135          140

tgc ggc gcc tgc tgg gcc ttc gcc gcc atc gcc acc gtg gag tcc atc      480
Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
145          150          155          160

tac aag atc aag aag ggc atc ctc gag ccg ctc tcc gag cag cag gtg      528
Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
          165          170          175

ctc gac tgc gcc aag ggc tac ggc tgc aag ggc ggc tgg gag ttc cgc      576

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Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 gcc ttc gag ttc atc atc tcc aac aag ggc gtg gcc tcc ggc gcc atc 624
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 tac ccg tac aag gcc gcc aag ggc acc tgc aag acc gac ggc gtg ccg 672
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 aac tcc gcc tac atc acc ggc tac gcc cgc gtg ccg cgc aac aac gag 720
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 tcc tcc atg atg tac gcc gtg tcc aag cag ccg atc acc gtg gcc gtg 768
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 gac gcc aac gcc aac ttc cag tac tac aag tcc ggc gtg ttc aac ggc 816
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270
 ccg tgc ggc acc tcc ctc aac cac gcc gtg acc gcc atc ggc tac ggc 864
 Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285
 cag gac tcc atc atc tac ccg aag aag tgg ggc gcc aag tgg ggc gag 912
 Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300
 gcc ggc tac atc cgc atg gcc cgc gac gtg tcc tcc tcc tcc ggc atc 960
 Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320
 tgc gcc atc gcc atc gac ccg ctc tac ccg acc ctc gag gag tag 1005
 Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 70
 <211> 334
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 70

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala Asp Glu Pro Ser Asp Pro
 20 25 30

Met Met Lys Arg Phe Glu Glu Trp Met Val Glu Tyr Gly Arg Val Tyr
 35 40 45
 Lys Asp Asn Asp Glu Lys Met Arg Arg Phe Gln Ile Phe Lys Asn Asn
 50 55 60
 Val Asn His Ile Glu Thr Phe Asn Ser Arg Asn Glu Asn Ser Tyr Thr
 65 70 75 80
 Leu Gly Ile Asn Gln Phe Thr Asp Met Thr Asn Asn Glu Phe Ile Ala
 85 90 95
 Gln Tyr Thr Gly Gly Ile Ser Arg Pro Leu Asn Ile Glu Arg Glu Pro
 100 105 110
 Val Val Ser Phe Asp Asp Val Asp Ile Ser Ala Val Pro Gln Ser Ile
 115 120 125
 Asp Trp Arg Asp Tyr Gly Ala Val Thr Ser Val Lys Asn Gln Asn Pro
 130 135 140
 Cys Gly Ala Cys Trp Ala Phe Ala Ala Ile Ala Thr Val Glu Ser Ile
 145 150 155 160
 Tyr Lys Ile Lys Lys Gly Ile Leu Glu Pro Leu Ser Glu Gln Gln Val
 165 170 175
 Leu Asp Cys Ala Lys Gly Tyr Gly Cys Lys Gly Gly Trp Glu Phe Arg
 180 185 190
 Ala Phe Glu Phe Ile Ile Ser Asn Lys Gly Val Ala Ser Gly Ala Ile
 195 200 205
 Tyr Pro Tyr Lys Ala Ala Lys Gly Thr Cys Lys Thr Asp Gly Val Pro
 210 215 220
 Asn Ser Ala Tyr Ile Thr Gly Tyr Ala Arg Val Pro Arg Asn Asn Glu
 225 230 235 240
 Ser Ser Met Met Tyr Ala Val Ser Lys Gln Pro Ile Thr Val Ala Val
 245 250 255
 Asp Ala Asn Ala Asn Phe Gln Tyr Tyr Lys Ser Gly Val Phe Asn Gly
 260 265 270

Pro Cys Gly Thr Ser Leu Asn His Ala Val Thr Ala Ile Gly Tyr Gly
 275 280 285

Gln Asp Ser Ile Ile Tyr Pro Lys Lys Trp Gly Ala Lys Trp Gly Glu
 290 295 300

Ala Gly Tyr Ile Arg Met Ala Arg Asp Val Ser Ser Ser Ser Gly Ile
 305 310 315 320

Cys Gly Ile Ala Ile Asp Pro Leu Tyr Pro Thr Leu Glu Glu
 325 330

<210> 71
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Bromealin signal sequence

<400> 71
 atggcctgga aggtgcaggt ggtgttctc ttctcttcc tctgcgtgat gtgggcctcc 60
 ccgtccgccc cctccgcc 78

<210> 72
 <211> 26
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Bromealin signal peptide

<400> 72

Met Ala Trp Lys Val Gln Val Val Phe Leu Phe Leu Phe Leu Cys Val
 1 5 10 15

Met Trp Ala Ser Pro Ser Ala Ala Ser Ala
 20 25

<210> 73
 <211> 1050
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11000

<400> 73
 atggcctgga aggtgcagggt ggtgttcctc ttctctctcc tctgcgtgat gtgggcctcc 60
 ccgtccgcgc cctccgcgga cgagccgtcc gaccgatga tgaagcgctt cgaggagtgg 120
 atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
 ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
 ctccgcatca accagttcac cgacatgacc aacaacgagt tcatcgcca gtacaccggc 300
 ggcattctcc gcccgctcaa catcgagcgc gagccggtgg tgccttcga cgacgtggac 360
 atctccgcgc tgcgcagtc catcgactgg cgcgactacg gcgcgtgac ctccgtgaag 420
 aaccagaacc cgtgcggcgc ctgctgggcc ttgcgcgcca tcgccaccgt ggagtcctc 480
 tacaagatca agaagggtcat cctcgagccg ctctccgagc agcaggtgct cgactgcgcc 540
 aagggtctac gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
 aagggcgtgg cctccgcgc catctaccg tacaaggccg ccaagggcac ctgcaagacc 660
 gacggcgtgc cgaactccgc ctacatcacc ggctacgcc gcgtgccgcg caacaacgag 720
 tcctccatga tgtacgccgt gtccaagcag ccgatcacc tggccgtgga cgccaacgcc 780
 aacttcagt actacaagtc cggcgtgttc aacggccgt gcggcacctc cctcaaccac 840
 gccgtgaccg ccacgcgcta cggccaggac tccatcatct accgaagaa gtggggcgcc 900
 aagtggggcg aggcgcgcta catccgatg gccgcgacg tgcctctc ctccggcatc 960
 tgcggcatcg ccacgaccc gctctaccg accctcgagg aggtgttcgc cgaggccatc 1020
 gccgccaact ccaccctcgt ggccgagtag . 1050

<210> 74
 <211> 1067
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11589

<400> 74
 tggcctggaa ggtgcagggt gtgttcctct ttctcttctc ctgcgtgatg tgggcctccc 60
 cgtccgcgc ctccgcctcc ttctctctct tcgccgactc caaccgatc cgcccggtga 120
 ccgaccgcgc cgctccacc gacgagccgt ccgaccgat gatgaagcgc ttcgaggagt 180
 ggatggtgga gtacggccgc gtgtacaagg acaacgacga gaagatgcgc cgcttcaga 240
 tcttcaagaa caacgtgaac cacatcgaga cttcaactc ccgcaacgag aactcctaca 300
 cctcggcat caaccagttc accgacatga ccaacaacga gttcatcgcc cagtacaccg 360

gcggcatctc ccgcccgcctc aacatcgagc gcgagccggt ggtgtccttc gacgacgtgg 420
 acatctccgc cgtgccgcag tccatcgact ggcgcgacta cggcgccgtg acctccgtga 480
 agaaccagaa cccgtgcggc gcctgctggg ccttcgccgc catcgccacc gtggagtcca 540
 tctacaagat caagaagggc atcctcgagc cgctctccga gcagcagggtg ctcgactgcg 600
 ccaagggcta cggctgcaag ggcggctggg agttccgcgc cttcgagttc atcatctcca 660
 acaagggcgt ggcctccggc gccatctacc cgtacaaggc cgccaagggc acctgcaaga 720
 ccgacggcgt gccgaactcc gcctacatca ccggctacgc ccgctgcccg cgcaacaacg 780
 agtctcccat gatgtacgcc gtgtccaagg agccgatcac cgtggccgtg gacgccaacg 840
 ccaacttcca gtactacaag tccggcgtgt tcaacggccc gtgcggcacc tccctcaacc 900
 acgccgtgac cgccatcggc tacggccagg actccatcat ctacccgaag aagtggggcg 960
 ccaagtgggg cgaggccggc tacatccgca tggcccgca cgtgtcctcc tctccggca 1020
 tctgcggcat cgccatcgac ccgctctacc cgaccctcga ggagtag 1067

<210> 75
 <211> 1023
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN11587 Sequence

<400> 75
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 ccgtccgccg cctccgcgga cgagccgtcc gacccgatga tgaagcgctt cgaggagtgg 120
 atggtggagt acggccgcgt gtacaaggac aacgacgaga agatgcgccg cttccagatc 180
 ttcaagaaca acgtgaacca catcgagacc ttcaactccc gcaacgagaa ctctacacc 240
 ctccgcatca accagttcac cgacatgacc aacaacgagt tcatcgccca gtacaccggc 300
 ggcattctcc gcccgctcaa catcgagcgc gagccggtgg tgtccttcga cgacgtggac 360
 atctccgccg tggcgagtc catcgactgg cgcgactacg gcgccgtgac ctccgtgaag 420
 aaccagaacc cgtgcggcgc ctgctgggccc ttccgcgcca tcgccaccgt ggagtcctac 480
 tacaagatca agaagggcatt cctcgagccg ctctccgagc agcagggtgct cgactgcgcc 540
 aagggttacg gctgcaaggg cggctgggag ttccgcgcct tcgagttcat catctccaac 600
 aagggcgtgg cctccggcgc catctacccg tacaaggccg ccaagggcac ctgcaagacc 660
 gacggcgtgc cgaactccgc ctacatcacc ggctacgccc gcgtgccgcg caacaacgag 720

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tcttccatga tgtacgccgt gtccaagcag ccgatcaccg tggccgtgga cgccaacgcc 780
aacttccagt actacaagtc cggcgtgttc aacggcccgt gcggcacctc cctcaaccac 840
gccgtgaccg ccatcggtta cggccaggac tccatcatct acccgaagaa gtggggcgcc 900
aagtggggcg aggcgggcta catccgcgtg gcccgcgacg tgctctcttc ctccggcatc 960
tgccggcatcg ccatcgaccc gctctaccgg accctcgagg agtccgagaa ggacgagctg 1020
tag 1023

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<210> 76
 <211> 990
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12169 Sequence

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<400> 76
atgagggtgt tgcctcgttc cctcgtcttc ctggctctcg ctgcgagcgc cacctccatg 60
gcggacgagc cgtccgaccc gatgatgaag cgcttcgagg agtggatggt ggagtacggc 120
cgcgtgtaca aggacaacga cgagaagatg cgcgccttc agatcttcaa gaacaacgtg 180
aaccacatcg agaccttcaa ctcccgcaac gagaactcct acaccctcgg catcaaccag 240
ttcaccgaca tgaccaacaa cgagttcatc gcccagtaca ccggcggcat ctcccgcccg 300
ctcaacatcg agcgcgagcc ggtggtgtcc ttcgacgacg tggacatctc cgccgtgccg 360
cagtcacatg actggcgaga ctacggcgcc gtgacctcgg tgaagaacca gaaccctgac 420
ggcgctcgtc gggccttcgc cgccatcgcc accgtggagt ccatctaaa gatcaagaag 480
ggcctcctcg agcgcgtctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 540
aaggcgcgct gggagtccg cgccctcgag ttcatcatct ccaacaaggg cgtggcctcc 600
ggcgccatct acccgtaaa ggccgccaag ggcacctgca agaccgacgg cgtgccgaac 660
tcgccttaca tcaccggcta cggccgctg ccgcgcaaca acgagtcctc catgatgtac 720
gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 780
aagtccggcg tgttcaacgg ccgctgcggc acctccctca accacgcgtg gaccgccatc 840
ggctacggcc aggactccat catctaccgg aagaagtggg gcgccaagtg gggcgaggcc 900
ggctacatcc gcatggcccg cgacgtgtcc tctcctcctc gcatctgcgg catcgccatc 960
gaaccgctct acccgacct cgaggagtag 990

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<210> 77
 <211> 1170
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSYN12575 Sequence

<400> 77
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 gacgcgtcca cgttcgcgcg cggcgccgcg cagggcctga ggggggcccg ggcgtcggcg 120
 gcggcggaaca cgttcagcat gcggaccagc gcgcgcgcgg cggccaggca ccagcaccag 180
 caggcgcccc ggggggcccag gttcccgtcg ctcgctcgtg gcgccagcgc cggcgccatg 240
 gcggacgagc cgtccgaccc gatgatgaag cgttcgagg agtggatggt ggagtacggc 300
 cgcgtgtaca aggacaacga cgagaagatg cgccgcttcc agatcttcaa gaacaacgtg 360
 aaccacatcg agaccttcaa ctcccgaac gagaactcct acacctcgg catcaaccag 420
 ttcaccgaca tgaccaacaa cgagttcatc gccagtaca ccggcggcat ctcccgcccg 480
 ctcaacatcg agcgcgagcc ggtggtgtcc ttgcagcagc tggacatctc cgcggtgccg 540
 cagtcacatc actgggcgga ctacggcgcc gtgacctcgg tgaagaacca gaaccctgc 600
 ggcgcctgct gggccttcgc cgccatcgcc accgtggagt ccatctaaa gatcaagaag 660
 ggcatectcg agccgctctc cgagcagcag gtgctcgact gcgccaaggg ctacggctgc 720
 aaggggcggt gggagttccg cgcttcgag ttcatcatct ccaacaaggg cgtggcctcc 780
 ggcgcctatc acccgtaaaa ggcgcgcaag ggcacctgca agaccgacgg cgtgccgaac 840
 tccgcctaca tcaccggcta cgcccgcggt cgcgcaaca acgagtctc catgatgtac 900
 gccgtgtcca agcagccgat caccgtggcc gtggacgcca acgccaactt ccagtactac 960
 aagtcggcg cgttcaacgg cccgtgcggc acctccctca accacgccgt gaccgccatc 1020
 ggctacggcc aggaactccat catctaccg aagaagtgg gcgccaagt gggcgaggcc 1080
 ggctacatcc gcatggccc cgacgtgtcc tctctctcc gcatctcgg catcgccatc 1140
 gaccgctct acccgacct cgaggagtag 1170

<210> 78
 <211> 1068
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSM270 Sequence

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<400> 78
atggcctgga aggtgcaggt ggtgttcttc ttctctttcc tctgctgat gtgggcctcc 60
ccgtccgcgc cctccgcctc ctctctctcc ttgcgcgact ccaaccgat ccgcccgtg 120
accgaccgcg ccgcctccac cgacgagccg tccgaccga tgatgaagcg cttcgaggag 180
tggatggtgg agtacggccg cgtgtacaag gacaacgacg agaagatgcg ccgcttccag 240
atcttcaaga acaacgtgaa ccacatcgag accttcaact cccgcaacga gaactctac 300
accttcggca tcaaccagtt caccgacatg accaacaacg agttcatcgc ccagtacacc 360
ggcggcatct cccgcccgtt caacatcgag cgcgagccgg tgggtgtcctt cgacgacgtg 420
gacatctccg ccgtgccgca gtccatcgac tggcgcgact acggcgccgt gacctccgtg 480
aagaaccaga acccgtgctg cgctgtctgg gccttcgccc ccatcgccac cgtggagtcc 540
atctacaaga tcaagaaggg catctctgag ccgctctccg agcagcaggt gctcgactgc 600
gccaaagggct acgggtgcaa gggcggtctg gagttccgcg ctttcgagtt catcatctcc 660
aacaagggcg tggcctccgg cgccatctac ccgtacaagg ccgccaaggg cacctgcaag 720
accgacggcg tggcgaactc cgctacatc accggctacg cccgctgcc gcgcaacaac 780
gagtcctcca tgatgtacgc cgtgtccaag cagccgatca ccgtggccgt ggacgccaac 840
gccaaacttcc agtactaaa gtccggcgtg ttcaacggcc cgtgcggcac ctccctcaac 900
cacgcccgtg ccgccatcgg ctacggccag gactccatca tctaccgaa gaagtggggc 960
gccaaagtgg gcgaggccgg ctacatccgc atggcccgcg acgtgtctc ctctccggc 1020
atctgcggca tcgccatcga cccgctctac ccgacctcg aggagtag 1068

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<210> 79
<211> 1497
<212> DNA
<213> Trichoderma reesei

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<220>
<221> CDS
<222> (1)..(1497)
<223> Trichoderma reesei cellobiohydrolase I

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<400> 79
atg cag tgc gcg tgt act ctc caa tgc gag act cac ccg cct ctg aca 48
Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
1 5 10 15

tgc cag aaa tgc tgc tct ggt ggc acg tgc act caa cag aca ggc tcc 96
Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

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gtg gtc atc gac gcc aac tgg cgc tgg act cac gct acg aac agc agc Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser 35 40 45	144
acg aac tgc tac gat ggc aac act tgg agc tcg acc cta tgt cct gac Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp 50 55 60	192
aac gag acc tgc gcg aag aac tgc tgt ctg gac ggt gcc gcc tac gcg Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala 65 70 75 80	240
tcc acg tac gga gtt acc acg agc ggt aac agc ctc tcc att ggc ttt Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe 85 90 95	288
gtc acc cag tct gcg cag aag aac gtt ggc gct cgc ctt tac ctt atg Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met 100 105 110	336
gcg agc gac acg acc tac cag gaa ttc acc ctg ctt ggc aac gag ttc Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe 115 120 125	384
tct ttc gat gtt gat gtt tcg cag ctg ccg tgc ggc ttg aac gga gct Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala 130 135 140	432
ctc tac ttc gtg tcc atg gac gcg gat ggt ggc gtg agc aag tat ccc Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro 145 150 155 160	480
acc aac acc gct ggc gcc aag tac ggc acg ggg tac tgt gac agc cag Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln 165 170 175	528
tgt ccc cgc gat ctg aag ttc atc aat ggc cag gcc aac gtt gag ggc Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly 180 185 190	576
tgg gag ccg tca tcc aac aac gcg aac acg ggc att gga gga cac gga Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly 195 200 205	624
agc tgc tgc tct gag atg gat atc tgg gag gcc aac tcc atc tcc gag Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu 210 215 220	672
gct ctt acc ccc cac cct tgc acg act gtc ggc cag gag atc tgc gag Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu 225 230 235 240	720
ggt gat ggg tgc ggc gga act tac tcc gat aac aga tat ggc ggc act Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr 245 250 255	768
tgc gat ccc gat ggc tgc gac tgg aac cca tac cgc ctg ggc aac acc Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr	816

260	265	270	
agc ttc tac ggc cct ggc tct Ser Phe Tyr Gly Pro Gly Ser 275	agc ttt acc ctc gat Ser Phe Thr Leu Asp 280	acc acc aag aaa Thr Thr Lys Lys 285	864
ttg acc gtt gtc acc cag ttc Leu Thr Val Val Thr Gln Phe 290	gag acg tcg ggt gcc atc aac cga tac Glu Thr Ser Gly Ala Ile Asn Arg Tyr 295	300	912
tat gtc cag aat ggc gtc act ttc cag cag ccc aac gcc gag ctt ggt Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly 305	310	315	960
agt tac tct ggc aac gag ctc aac gat gat tac tgc aca gct gag gag Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu 325	330	335	1008
gca gaa ttc ggc gga tcc tct ttc tca gac aag ggc gcc ctg act cag Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln 340	345	350	1056
ttc aag aag gct acc tct ggc ggc atg gtt ctg gtc atg agt ctg tgg Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp 355	360	365	1104
gat gat tac tac gcc aac atg ctg tgg ctg gac tcc acc tac ccg aca Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr 370	375	380	1152
aac gag acc tcc tcc aca ccc ggt gcc gtg cgc gga agc tgc tcc acc Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr 385	390	395	1200
agc tcc ggt gtc cct gct cag gtc gaa tct cag tct ccc aac gcc aag Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys 405	410	415	1248
gtc acc ttc tcc aac atc aag ttc gga ccc att ggc agc acc ggc aac Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn 420	425	430	1296
cct agc ggc ggc aac cct ccc ggc gga aac ccg cct ggc acc acc acc Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr 435	440	445	1344
acc cgc cgc cca gcc act acc act gga agc tct ccc gga cct acc cag Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln 450	455	460	1392
tct cac tac ggc cag tgc ggc ggt att ggc tac agc ggc ccc acg gtc Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val 465	470	475	1440
tgc gcc agc ggc aca act tgc cag gtc ctg aac cct tac tac tct cag Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln 485	490	495	1488

tgc ctg taa
Cys Leu

1497

<210> 80
<211> 498
<212> PRT
<213> Trichoderma reesei

<400> 80

Met Gln Ser Ala Cys Thr Leu Gln Ser Glu Thr His Pro Pro Leu Thr
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Trp Gln Lys Cys Ser Ser Gly Gly Thr Cys Thr Gln Gln Thr Gly Ser
20 25 30

Val Val Ile Asp Ala Asn Trp Arg Trp Thr His Ala Thr Asn Ser Ser
35 40 45

Thr Asn Cys Tyr Asp Gly Asn Thr Trp Ser Ser Thr Leu Cys Pro Asp
50 55 60

Asn Glu Thr Cys Ala Lys Asn Cys Cys Leu Asp Gly Ala Ala Tyr Ala
65 70 75 80

Ser Thr Tyr Gly Val Thr Thr Ser Gly Asn Ser Leu Ser Ile Gly Phe
85 90 95

Val Thr Gln Ser Ala Gln Lys Asn Val Gly Ala Arg Leu Tyr Leu Met
100 105 110

Ala Ser Asp Thr Thr Tyr Gln Glu Phe Thr Leu Leu Gly Asn Glu Phe
115 120 125

Ser Phe Asp Val Asp Val Ser Gln Leu Pro Cys Gly Leu Asn Gly Ala
130 135 140

Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Val Ser Lys Tyr Pro
145 150 155 160

Thr Asn Thr Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
165 170 175

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
180 185 190

Trp Glu Pro Ser Ser Asn Asn Ala Asn Thr Gly Ile Gly Gly His Gly
 195 200 205
 Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Glu
 210 215 220
 Ala Leu Thr Pro His Pro Cys Thr Thr Val Gly Gln Glu Ile Cys Glu
 225 230 235 240
 Gly Asp Gly Cys Gly Gly Thr Tyr Ser Asp Asn Arg Tyr Gly Gly Thr
 245 250 255
 Cys Asp Pro Asp Gly Cys Asp Trp Asn Pro Tyr Arg Leu Gly Asn Thr
 260 265 270
 Ser Phe Tyr Gly Pro Gly Ser Ser Phe Thr Leu Asp Thr Thr Lys Lys
 275 280 285
 Leu Thr Val Val Thr Gln Phe Glu Thr Ser Gly Ala Ile Asn Arg Tyr
 290 295 300
 Tyr Val Gln Asn Gly Val Thr Phe Gln Gln Pro Asn Ala Glu Leu Gly
 305 310 315 320
 Ser Tyr Ser Gly Asn Glu Leu Asn Asp Asp Tyr Cys Thr Ala Glu Glu
 325 330 335
 Ala Glu Phe Gly Gly Ser Ser Phe Ser Asp Lys Gly Gly Leu Thr Gln
 340 345 350
 Phe Lys Lys Ala Thr Ser Gly Gly Met Val Leu Val Met Ser Leu Trp
 355 360 365
 Asp Asp Tyr Tyr Ala Asn Met Leu Trp Leu Asp Ser Thr Tyr Pro Thr
 370 375 380
 Asn Glu Thr Ser Ser Thr Pro Gly Ala Val Arg Gly Ser Cys Ser Thr
 385 390 395 400
 Ser Ser Gly Val Pro Ala Gln Val Glu Ser Gln Ser Pro Asn Ala Lys
 405 410 415

Val Thr Phe Ser Asn Ile Lys Phe Gly Pro Ile Gly Ser Thr Gly Asn
420 425 430

Pro Ser Gly Gly Asn Pro Pro Gly Gly Asn Pro Pro Gly Thr Thr Thr
435 440 445

Thr Arg Arg Pro Ala Thr Thr Thr Gly Ser Ser Pro Gly Pro Thr Gln
450 455 460

Ser His Tyr Gly Gln Cys Gly Gly Ile Gly Tyr Ser Gly Pro Thr Val
465 470 475 480

Cys Ala Ser Gly Thr Thr Cys Gln Val Leu Asn Pro Tyr Tyr Ser Gln
485 490 495

Cys Leu

<210> 31
<211> 1365
<212> DNA
<213> Trichoderma reesei

<220>
<221> CDS
<222> (1)..(1365)
<223> trichoderma reesei cellobiohydrolase II

<400> 81
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tgt ggt ggc cag aat tgg tcg ggt ccg act tgc tgt gct tcc gga agc 96
Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
20 25 30
aca tgc gtc tac tcc aac gac tat tac tcc cag tgt ctt ccc ggc gct 144
Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
35 40 45
gca agc tca agc tcg tcc acg cgc gcc gcg tcg acg act tca cga gta 192
Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
50 55 60
tcc ccc aca aca tcc cgg tcg agc tcc gcg acg cct cca cct ggt tct 240
Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
65 70 75 80
acc act acc aga gta cct cca gtc gga tcg gga acc gct acg tat tca 288
Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser

85	90	95	
ggc aac cct ttt gtt ggg gtc act cct tgg gcc aat gca tat tac gcc Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala 100 105 110			336
tct gaa gtt agc agc ctc gct att cct agc ttg act gga gcc atg gcc Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala 115 120 125			384
act gct gca gca gct gtc gca aag gtt ccc tct ttt atg tgg cta gat Thr Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp 130 135 140			432
act ctt gac aag acc cct ctc atg gag caa acc ttg gcc gac atc cgc Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg 145 150 155 160			480
acc gcc aac aag aat ggc ggt aac tat gcc gga cag ttt gtg gtg tat Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr 165 170 175			528
gac ttg ccg gat cgc gat tgc gct gcc ctt gcc tcg aat ggc gaa tac Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr 180 185 190			576
tct att gcc gat ggt ggc gtc gcc aaa tat aag aac tat atc gac acc Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr 195 200 205			624
att cgt caa att gtc gtg gaa tat tcc gat atc cgg acc ctc ctg gtt Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val 210 215 220			672
att gag cct gac tct ctt gcc aac ctg gtg acc aac ctc ggt act cca Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro 225 230 235 240			720
aag tgt gcc aat gct cag tca gcc tac ctt gag tgc atc aac tac gcc Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala 245 250 255			768
gtc aca cag ctg aac ctt cca aat gtt gcg atg tat ttg gac gct ggc Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly 260 265 270			816
cat gca gga tgg ctt ggc tgg ccg gca aac caa gac ccg gcc gct cag His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln 275 280 285			864
cta ttt gca aat gtt tac aag aat gca tcg tct ccg aga gct ctt cgc Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg 290 295 300			912
gga ttg gca acc aat gtc gcc aac tac aac ggg tgg aac att acc agc Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser 305 310 315 320			960

ccc cca tcg tac acg caa ggc aac gct gtc tac aac gag aag ctg tac 1008
 Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
 325 330 335
 atc cac gct att gga cct ctt ctt gcc aat cac ggc tgg tcc aac gcc 1056
 Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
 340 345 350
 ttc ttc atc act gat caa ggt cga tcg gga aag cag cct acc gga cag 1104
 Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
 355 360 365
 caa cag tgg gga gac tgg tgc aat gtg atc ggc acc gga ttt ggt att 1152
 Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
 370 375 380
 cgc cca tcc gca aac act ggg gac tcg ttg ctg gat tcg ttt gtc tgg 1200
 Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
 395 390 395 400
 gtc aag cca ggc ggc gag tgt gac ggc acc agc gac agc agt gcg cca 1248
 Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
 405 410 415
 cga ttt gac tcc cac tgt gcg ctc cca gat gcc ttg caa ccg gcg cct 1296
 Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
 420 425 430
 caa gct ggt gct tgg ttc caa gcc tac ttt gtg cag ctt ctc aca aac 1344
 Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
 435 440 445
 gca aac cca tcg ttc ctg tag 1365
 Ala Asn Pro Ser Phe Leu
 450

<210> 52
 <211> 454
 <212> PRT
 <213> Trichoderma reesei

<400> 82

Met Val Pro Leu Glu Glu Arg Gln Ala Cys Ser Ser Val Trp Gly Gln
 1 5 10 15
 Cys Gly Gly Gln Asn Trp Ser Gly Pro Thr Cys Cys Ala Ser Gly Ser
 20 25 30
 Thr Cys Val Tyr Ser Asn Asp Tyr Tyr Ser Gln Cys Leu Pro Gly Ala
 35 40 45
 Ala Ser Ser Ser Ser Ser Thr Arg Ala Ala Ser Thr Thr Ser Arg Val
 50 55 60

Ser Pro Thr Thr Ser Arg Ser Ser Ser Ala Thr Pro Pro Pro Gly Ser
 65 70 75 80
 Thr Thr Thr Arg Val Pro Pro Val Gly Ser Gly Thr Ala Thr Tyr Ser
 85 90 95
 Gly Asn Pro Phe Val Gly Val Thr Pro Trp Ala Asn Ala Tyr Tyr Ala
 100 105 110
 Ser Glu Val Ser Ser Leu Ala Ile Pro Ser Leu Thr Gly Ala Met Ala
 115 120 125
 Thr Ala Ala Ala Ala Val Ala Lys Val Pro Ser Phe Met Trp Leu Asp
 130 135 140
 Thr Leu Asp Lys Thr Pro Leu Met Glu Gln Thr Leu Ala Asp Ile Arg
 145 150 155 160
 Thr Ala Asn Lys Asn Gly Gly Asn Tyr Ala Gly Gln Phe Val Val Tyr
 165 170 175
 Asp Leu Pro Asp Arg Asp Cys Ala Ala Leu Ala Ser Asn Gly Glu Tyr
 180 185 190
 Ser Ile Ala Asp Gly Gly Val Ala Lys Tyr Lys Asn Tyr Ile Asp Thr
 195 200 205
 Ile Arg Gln Ile Val Val Glu Tyr Ser Asp Ile Arg Thr Leu Leu Val
 210 215 220
 Ile Glu Pro Asp Ser Leu Ala Asn Leu Val Thr Asn Leu Gly Thr Pro
 225 230 235 240
 Lys Cys Ala Asn Ala Gln Ser Ala Tyr Leu Glu Cys Ile Asn Tyr Ala
 245 250 255
 Val Thr Gln Leu Asn Leu Pro Asn Val Ala Met Tyr Leu Asp Ala Gly
 260 265 270
 His Ala Gly Trp Leu Gly Trp Pro Ala Asn Gln Asp Pro Ala Ala Gln
 275 280 285

Leu Phe Ala Asn Val Tyr Lys Asn Ala Ser Ser Pro Arg Ala Leu Arg
 290 295 300

Gly Leu Ala Thr Asn Val Ala Asn Tyr Asn Gly Trp Asn Ile Thr Ser
 305 310 315 320

Pro Pro Ser Tyr Thr Gln Gly Asn Ala Val Tyr Asn Glu Lys Leu Tyr
 325 330 335

Ile His Ala Ile Gly Pro Leu Leu Ala Asn His Gly Trp Ser Asn Ala
 340 345 350

Phe Phe Ile Thr Asp Gln Gly Arg Ser Gly Lys Gln Pro Thr Gly Gln
 355 360 365

Gln Gln Trp Gly Asp Trp Cys Asn Val Ile Gly Thr Gly Phe Gly Ile
 370 375 380

Arg Pro Ser Ala Asn Thr Gly Asp Ser Leu Leu Asp Ser Phe Val Trp
 385 390 395 400

Val Lys Pro Gly Gly Glu Cys Asp Gly Thr Ser Asp Ser Ser Ala Pro
 405 410 415

Arg Phe Asp Ser His Cys Ala Leu Pro Asp Ala Leu Gln Pro Ala Pro
 420 425 430

Gln Ala Gly Ala Trp Phe Gln Ala Tyr Phe Val Gln Leu Leu Thr Asn
 435 440 445

Ala Asn Pro Ser Phe Leu
 450

<210> 83
 <211> 1317
 <212> DNA
 <213> Trichoderma reesei

<220>
 <221> CDS
 <222> (1)..(1317)
 <223> Trichoderma reesei endoglucanase I

<400> 83
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 Met Gln Gln Pro Gly Thr Ser Thr Pro Glu Val His Pro Lys Leu Thr

48

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acc tac aag tgc aca aag tcc ggg ggg tgc gtg gcc cag gac acc tcg	96			
Thr Tyr Lys Cys Thr Lys Ser Gly Gly Cys Val Ala Gln Asp Thr Ser				
20 25 30				
gtg gtc ctt gac tgg aac tac cgc tgg atg cac gac gca aac tac aac	144			
Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn				
35 40 45				
tcg tgc acc gtc aac ggc ggc gtc aac acc acg ctc tgc cct gac gag	192			
Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu				
50 55 60				
gcg acc tgt ggc aag aac tgc ttc atc gag ggc gtc gac tac gcc gcc	240			
Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala				
65 70 75 80				
tcg ggc gtc acg acc tcg ggc agc agc ctc acc atg aac cag tac atg	288			
Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met				
85 90 95				
ccc agc agc tct ggc ggc tac agc agc gtc tct cct cgg ctg tat ctc	336			
Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu				
100 105 110				
ctg gac tct gac ggt gag tac gtg atg ctg aag ctc aac ggc cag gag	384			
Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu				
115 120 125				
ctg agc ttc gac gtc gac ctc tct gct ctg ccg tgt gga gag aac ggc	432			
Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly				
130 135 140				
tcg ctc tac ctg tct cag atg gac gag aac ggg ggc gcc aac cag tat	480			
Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr				
145 150 155 160				
aac acg gcc ggt gcc aac tac ggg agc ggc tac tgc gat gct cag tgc	528			
Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys				
165 170 175				
ccc gtc cag aca tgg agg aac ggc acc ctc aac act agc cac cag ggc	576			
Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly				
180 185 190				
ttc tgc tgc aac gag atg gat atc ctg gag ggc aac tcg agg gcg aat	624			
Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn				
195 200 205				
gcc ttg acc cct cac tct tgc acg gcc acg gcc tgc gac tct gcc ggt	672			
Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly				
210 215 220				
tgc ggc ttc aac ccc tat ggc agc ggc tac aaa agc tac tac ggc ccc	720			
Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro				
225 230 235 240				

gga gat acc gtt gac acc tcc aag acc ttc acc atc atc acc cag ttc 768
 Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
 245 250 255

aac acg gac aac ggc tcg ccc tcg ggc aac ctt gtg agc atc acc cgc 816
 Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
 260 265 270

aag tac cag caa aac ggc gtc gac atc ccc agc gcc cag ccc ggc ggc 864
 Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
 275 280 285

gac acc atc tcg tcc tgc ccg tcc gcc tca gcc tac ggc ggc ctc gcc 912
 Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
 290 295 300

acc atg ggc aag gcc ctg agc agc ggc atg gtg ctc gtg ttc agc att 960
 Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
 305 310 315 320

tgg aac gac aac agc cag tac atg aac tgg ctc gac agc ggc aac gcc 1008
 Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
 325 330 335

ggc ccc tgc agc agc acc gag ggc aac cca tcc aac acc ctg gcc aac 1056
 Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
 340 345 350

aac ccc aac acg cac gtc gtc ttc tcc aac atc cgc tgg gga gac att 1104
 Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
 355 360 365

ggg tct act acg aac tcg act gcg ccc ccg ccc ccg cct gcg tcc agc 1152
 Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
 370 375 380

acg acg ttt tcg act aca cgg agg agc tcg acg act tcg agc agc ccg 1200
 Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Pro
 385 390 395 400

agc tgc acg cag act cac tgg ggg cag tgc ggt ggc att ggg tac agc 1248
 Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
 405 410 415

ggg tgc aag acg tgc acg tcg ggc act acg tgc cag tat agc aac gac 1296
 Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
 420 425 430

tac tac tcg caa tgc ctt tag 1317
 Tyr Tyr Ser Gln Cys Leu
 435

<210> 84
 <211> 438
 <212> PRT
 <213> Trichoderma reesei

<400> 84

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20          25          30

Val Val Leu Asp Trp Asn Tyr Arg Trp Met His Asp Ala Asn Tyr Asn
35          40          45

Ser Cys Thr Val Asn Gly Gly Val Asn Thr Thr Leu Cys Pro Asp Glu
50          55          60

Ala Thr Cys Gly Lys Asn Cys Phe Ile Glu Gly Val Asp Tyr Ala Ala
65          70          75          80

Ser Gly Val Thr Thr Ser Gly Ser Ser Leu Thr Met Asn Gln Tyr Met
85          90          95

Pro Ser Ser Ser Gly Gly Tyr Ser Ser Val Ser Pro Arg Leu Tyr Leu
100         105         110

Leu Asp Ser Asp Gly Glu Tyr Val Met Leu Lys Leu Asn Gly Gln Glu
115         120         125

Leu Ser Phe Asp Val Asp Leu Ser Ala Leu Pro Cys Gly Glu Asn Gly
130         135         140

Ser Leu Tyr Leu Ser Gln Met Asp Glu Asn Gly Gly Ala Asn Gln Tyr
145         150         155         160

Asn Thr Ala Gly Ala Asn Tyr Gly Ser Gly Tyr Cys Asp Ala Gln Cys
165         170         175

Pro Val Gln Thr Trp Arg Asn Gly Thr Leu Asn Thr Ser His Gln Gly
180         185         190

Phe Cys Cys Asn Glu Met Asp Ile Leu Glu Gly Asn Ser Arg Ala Asn
195         200         205

Ala Leu Thr Pro His Ser Cys Thr Ala Thr Ala Cys Asp Ser Ala Gly
210         215         220

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Cys Gly Phe Asn Pro Tyr Gly Ser Gly Tyr Lys Ser Tyr Tyr Gly Pro
 225 230 235 240
 Gly Asp Thr Val Asp Thr Ser Lys Thr Phe Thr Ile Ile Thr Gln Phe
 245 250 255
 Asn Thr Asp Asn Gly Ser Pro Ser Gly Asn Leu Val Ser Ile Thr Arg
 260 265 270
 Lys Tyr Gln Gln Asn Gly Val Asp Ile Pro Ser Ala Gln Pro Gly Gly
 275 280 285
 Asp Thr Ile Ser Ser Cys Pro Ser Ala Ser Ala Tyr Gly Gly Leu Ala
 290 295 300
 Thr Met Gly Lys Ala Leu Ser Ser Gly Met Val Leu Val Phe Ser Ile
 305 310 315 320
 Trp Asn Asp Asn Ser Gln Tyr Met Asn Trp Leu Asp Ser Gly Asn Ala
 325 330 335
 Gly Pro Cys Ser Ser Thr Glu Gly Asn Pro Ser Asn Thr Leu Ala Asn
 340 345 350
 Asn Pro Asn Thr His Val Val Phe Ser Asn Ile Arg Trp Gly Asp Ile
 355 360 365
 Gly Ser Thr Thr Asn Ser Thr Ala Pro Pro Pro Pro Pro Ala Ser Ser
 370 375 380
 Thr Thr Phe Ser Thr Thr Arg Arg Ser Ser Thr Thr Ser Ser Ser Pro
 385 390 395 400
 Ser Cys Thr Gln Thr His Trp Gly Gln Cys Gly Gly Ile Gly Tyr Ser
 405 410 415
 Gly Cys Lys Thr Cys Thr Ser Gly Thr Thr Cys Gln Tyr Ser Asn Asp
 420 425 430
 Tyr Tyr Ser Gln Cys Leu
 435

<210> 85
 <211> 954

<212> DNA
 <213> Artificial Sequence

<220>
 <223> 6GP1

<220>
 <221> CDS
 <222> (1)..(954)
 <223> 6GP1

<400> 85
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 aac atc ggc aac gcc ctg gag gcc ccg aac gag ggc gac tgg ggc gtg 96
 Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
 20 25 30
 gtg atc aag gac gag ttc ttc gac atc atc aag gag gcc ggc ttc tcc 144
 Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
 35 40 45
 cac gtg cgc atc ccg atc cgc tgg tcc acc cac gcc tac gcc ttc ccg 192
 His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60
 ccg tac aag atc atg gac cgc ttc ttc aag cgc gtg gac gag gtg atc 240
 Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80
 aac ggc gcc ctc aag cgc ggc ctc gcc gtg gcc atc aac atc cac cac 288
 Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95
 tac gag gag ctc atg aac gac ccg gag gag cac aag gag cgc ttc ctc 336
 Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110
 gcc ctc tgg aag cag atc gcc gac cgc tac aag gac tac ccg gag acc 384
 Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125
 ctc ttc ttc gag atc ctc aac gag ccg cac ggc aac ctc acc ccg gag 432
 Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
 130 135 140
 aag tgg aac gag ctg ctc gag gag gcc ctc aag gtg atc cgc tcc atc 480
 Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
 145 150 155 160
 gac aag aag cac acc atc atc att ggc acc gca gag tgg gga ggc atc 528
 Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
 165 170 175
 tcc gcc ctc gag aag ctc tcc gtg ccg aag tgg gag aag aat tcc atc 576

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Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
      180                      185                      190

gtg acc atc cac tac tac aac ccg ttc gag ttc acg cac cag ggc gcc      624
Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
      195                      200                      205

gag tgg gtg gag ggc tcc gag aag tgg ctt ggc cgc aag tgg ggc tcc      672
Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
      210                      215                      220

ccg gac gac cag aag cac ctc atc gag gag ttc aac ttc atc gag gag      720
Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
      225                      230                      235

tgg tcc aag aag aac aag cgc ccg atc tac atc ggc gag ttt ggc gcc      768
Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
      245                      250                      255

tac cgc aag gcc gac ctc gag tcc cgc atc aag tgg acc tcc ttc gtg      816
Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
      260                      265                      270

gtg cgt gag atg gag aag cgc cgc tgg tcc tgg gcc tac tgg gag ttc      864
Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
      275                      280                      285

tgc tcc ggc ttc ggc gtg tac gac acc ctc cgc aag acc tgg aac aag      912
Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
      290                      295                      300

gac ctc ctc gag gcc ctc atc ggc ggc gac tcc atc gag tag      954
Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
      305                      310                      315

<210> 86
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 86

Met Gly Val Asp Pro Phe Glu Arg Asn Lys Ile Leu Gly Arg Gly Ile
1      5      10      15

Asn Ile Gly Asn Ala Leu Glu Ala Pro Asn Glu Gly Asp Trp Gly Val
20      25      30

Val Ile Lys Asp Glu Phe Phe Asp Ile Ile Lys Glu Ala Gly Phe Ser
35      40      45

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His Val Arg Ile Pro Ile Arg Trp Ser Thr His Ala Tyr Ala Phe Pro
 50 55 60

Pro Tyr Lys Ile Met Asp Arg Phe Phe Lys Arg Val Asp Glu Val Ile
 65 70 75 80

Asn Gly Ala Leu Lys Arg Gly Leu Ala Val Ala Ile Asn Ile His His
 85 90 95

Tyr Glu Glu Leu Met Asn Asp Pro Glu Glu His Lys Glu Arg Phe Leu
 100 105 110

Ala Leu Trp Lys Gln Ile Ala Asp Arg Tyr Lys Asp Tyr Pro Glu Thr
 115 120 125

Leu Phe Phe Glu Ile Leu Asn Glu Pro His Gly Asn Leu Thr Pro Glu
 130 135 140

Lys Trp Asn Glu Leu Leu Glu Glu Ala Leu Lys Val Ile Arg Ser Ile
 145 150 155 160

Asp Lys Lys His Thr Ile Ile Ile Gly Thr Ala Glu Trp Gly Gly Ile
 165 170 175

Ser Ala Leu Glu Lys Leu Ser Val Pro Lys Trp Glu Lys Asn Ser Ile
 180 185 190

Val Thr Ile His Tyr Tyr Asn Pro Phe Glu Phe Thr His Gln Gly Ala
 195 200 205

Glu Trp Val Glu Gly Ser Glu Lys Trp Leu Gly Arg Lys Trp Gly Ser
 210 215 220

Pro Asp Asp Gln Lys His Leu Ile Glu Glu Phe Asn Phe Ile Glu Glu
 225 230 235 240

Trp Ser Lys Lys Asn Lys Arg Pro Ile Tyr Ile Gly Glu Phe Gly Ala
 245 250 255

Tyr Arg Lys Ala Asp Leu Glu Ser Arg Ile Lys Trp Thr Ser Phe Val
 260 265 270

Val Arg Glu Met Glu Lys Arg Arg Trp Ser Trp Ala Tyr Trp Glu Phe
 275 280 285

Cys Ser Gly Phe Gly Val Tyr Asp Thr Leu Arg Lys Thr Trp Asn Lys
 290 295 300

Asp Leu Leu Glu Ala Leu Ile Gly Gly Asp Ser Ile Glu
 305 310 315

<210> 87
 <211> 1248
 <212> DNA
 <213> Hordeum vulgare

<220>
 <221> CDS
 <222> (1)..(1248)
 <223> Barley AmyI amylase

<400> 87
 atg gca cac caa gtc ctc ttt cag ggg ttc aac tgg gag tcg tgg aag 48
 Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15
 cag agc ggc ggg tgg tac aac atg atg atg ggc aag gtc gac gac atc 96
 Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30
 gcc gct gcc gga gtc acc cac gtc tgg ctg cca ccg ccg tcg cac tcc 144
 Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45
 gtc tcc aac gaa ggt tac atg cct ggt cgg ctg tac gac atc gac gcg 192
 Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60
 tcc aag tac ggc aac gcg gcg gag ctc aag tcg ctc atc ggc gcg ctc 240
 Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 65 70 75 80
 cac ggc aag ggc gtg cag gcc atc gcc gac atc gtc atc aac cac cgc 288
 His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
 85 90 95
 tgc gcc gac tac aag gat agc cgc ggc atc tac tgc atc ttc gag ggc 336
 Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
 100 105 110
 ggc acc tcc gac ggc cgc ctc gac tgg ggc ccc cac atg atc tgt cgc 384
 Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
 115 120 125
 gac gac acc aaa tac tcc gat ggc acc gca aac ctc gac acc gga gcc 432
 Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
 130 135 140

gac ttc gcc gcc gcg ccc gac atc gac cac ctc aac gac cgg gtc cag Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln 145 150 155 160	480
cgc gag ctc aag gag tgg ctc ctc tgg ctc aag agc gac ctc ggc ttc Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe 165 170 175	528
gac gcg tgg cgc ctt gac ttc gcc agg ggc tac tcg ccg gag atg gcc Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala 180 185 190	576
aag gtg tac atc gac ggc aca tcc ccg agc ctc gcc gtg gcc gag gtg Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val 195 200 205	624
tgg gac aat atg gcc acc ggc ggc gac ggc aag ccc aac tac gac cag Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln 210 215 220	672
gac gcg cac cgg cag aat ctg gtg aac tgg gtg gac aag gtg ggc ggc Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly 225 230 235 240	720
gcg gcc tcg gca ggc atg gtg ttc gac ttc acg acc aaa ggg ata ctg Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu 245 250 255	768
aac gct gcc gtg gag ggc gag ctg tgg agg ctg atc gac ccg cag ggg Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly 260 265 270	816
aag gcc ccc ggc gtg atg gga tgg tgg ccg gcc aag gcc gtc acc ttc Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe 275 280 285	864
gtc gac aac cac gat aca ggc tcc acg cag gcc atg tgg cca ttc ccc Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro 290 295 300	912
tcc gac aag gtc atg cag ggc tac gcg tac atc ctc acc cac ccc ggc Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly 305 310 315 320	960
atc cca tgc atc ttc tac gac cat ttc ttc aac tgg ggg ttt aag gac Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp 325 330 335	1008
cag atc gcg gcg ctg gtg gcg atc agg aag cgc aac ggc atc acg gcg Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala 340 345 350	1056
acg agc gct ctg aag atc ctc atg cac gaa gga gat gcc tac gtc gcc Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala 355 360 365	1104
gag ata gac ggc aag gtg gtg gtg aag atc ggg tcc agg tac gac gtc Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val	1152

370 375 380
 ggg gcg gtg atc ccg gcc ggg ttc gtg acc tcg gca cac ggc aac gac 1200
 Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400
 tac gcc gtc tgg gag aag aac ggt gcc gcg gca aca cta caa cgg agc 1248
 Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Thr Leu Gln Arg Ser
 405 410 415

 <210> 88
 <211> 416
 <212> PRT
 <213> Hordeum vulgare

 <400> 88
 Met Ala His Gln Val Leu Phe Gln Gly Phe Asn Trp Glu Ser Trp Lys
 1 5 10 15
 Gln Ser Gly Gly Trp Tyr Asn Met Met Met Gly Lys Val Asp Asp Ile
 20 25 30
 Ala Ala Ala Gly Val Thr His Val Trp Leu Pro Pro Pro Ser His Ser
 35 40 45
 Val Ser Asn Glu Gly Tyr Met Pro Gly Arg Leu Tyr Asp Ile Asp Ala
 50 55 60
 Ser Lys Tyr Gly Asn Ala Ala Glu Leu Lys Ser Leu Ile Gly Ala Leu
 65 70 75 80
 His Gly Lys Gly Val Gln Ala Ile Ala Asp Ile Val Ile Asn His Arg
 85 90 95
 Cys Ala Asp Tyr Lys Asp Ser Arg Gly Ile Tyr Cys Ile Phe Glu Gly
 100 105 110
 Gly Thr Ser Asp Gly Arg Leu Asp Trp Gly Pro His Met Ile Cys Arg
 115 120 125
 Asp Asp Thr Lys Tyr Ser Asp Gly Thr Ala Asn Leu Asp Thr Gly Ala
 130 135 140
 Asp Phe Ala Ala Ala Pro Asp Ile Asp His Leu Asn Asp Arg Val Gln
 145 150 155 160

Arg Glu Leu Lys Glu Trp Leu Leu Trp Leu Lys Ser Asp Leu Gly Phe
 165 170 175
 Asp Ala Trp Arg Leu Asp Phe Ala Arg Gly Tyr Ser Pro Glu Met Ala
 180 185 190
 Lys Val Tyr Ile Asp Gly Thr Ser Pro Ser Leu Ala Val Ala Glu Val
 195 200 205
 Trp Asp Asn Met Ala Thr Gly Gly Asp Gly Lys Pro Asn Tyr Asp Gln
 210 215 220
 Asp Ala His Arg Gln Asn Leu Val Asn Trp Val Asp Lys Val Gly Gly
 225 230 235 240
 Ala Ala Ser Ala Gly Met Val Phe Asp Phe Thr Thr Lys Gly Ile Leu
 245 250 255
 Asn Ala Ala Val Glu Gly Glu Leu Trp Arg Leu Ile Asp Pro Gln Gly
 260 265 270
 Lys Ala Pro Gly Val Met Gly Trp Trp Pro Ala Lys Ala Val Thr Phe
 275 280 285
 Val Asp Asn His Asp Thr Gly Ser Thr Gln Ala Met Trp Pro Phe Pro
 290 295 300
 Ser Asp Lys Val Met Gln Gly Tyr Ala Tyr Ile Leu Thr His Pro Gly
 305 310 315 320
 Ile Pro Cys Ile Phe Tyr Asp His Phe Phe Asn Trp Gly Phe Lys Asp
 325 330 335
 Gln Ile Ala Ala Leu Val Ala Ile Arg Lys Arg Asn Gly Ile Thr Ala
 340 345 350
 Thr Ser Ala Leu Lys Ile Leu Met His Glu Gly Asp Ala Tyr Val Ala
 355 360 365
 Glu Ile Asp Gly Lys Val Val Val Lys Ile Gly Ser Arg Tyr Asp Val
 370 375 380
 Gly Ala Val Ile Pro Ala Gly Phe Val Thr Ser Ala His Gly Asn Asp
 385 390 395 400

Tyr Ala Val Trp Glu Lys Asn Gly Ala Ala Ala Thr Leu Gln Arg Ser
 405 410 415

<210> 89
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Trichoderma reesei β -Glucosidase 2

<220>
 <221> CDS
 <222> (1)..(1401)
 <223> Trichoderma reesei β -Glucosidase 2

<400> 89
 atg ttg ccc aag gac ttt cag tgg ggg ttc gcc acg gct gcc tac cag 48
 Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
 1 5 10 15
 atc gag ggc gcc gtc gac cag gac ggc cgc ggc ccc agc atc tgg gac 96
 Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
 20 25 30
 acg ttc tgc gcg cag ccc ggc aag atc gcc gac ggc tcg tcg ggc gtg 144
 Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
 35 40 45
 acg gcg tgc gac tcg tac aac cgc acg gcc gag gac att gcg ctg ctg 192
 Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
 50 55 60
 aag tcg ctc ggg gcc aag agc tac cgc ttc tcc atc tcg tgg tcg cgc 240
 Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
 65 70 75 80
 atc atc ccc gag ggc ggc cgc ggc gat gcc gtc aac cag gcg ggc atc 288
 Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
 85 90 95
 gac cac tac gtc aag ttc gtc gac gac ctg ctc gac gcc ggc atc acg 336
 Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
 100 105 110
 ccc ttc atc acc ctc ttc cac tgg gac ctg ccc gag ggc ctg cat cag 384
 Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
 115 120 125
 cgg tac ggg ggg ctg ctg aac cgc acc gag ttc ccg ctc gac ttt gaa 432
 Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
 130 135 140
 aac tac gcc cgc gtc atg ttc agg gcg ctg ccc aag gtg cgc aac tgg 480

Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp	
145 150 155 160	
atc acc ttc aac gag ccg ctg tgc tgc gcc atc ccg ggc tac ggc tcc	528
Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser	
165 170 175	
ggc acc ttc gcc ccc ggc cgg cag agc acc tcg gag ccg tgg acc gtc	576
Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val	
180 185 190	
ggc cac aac atc ctg gtc gcc cac ggc cgc gcc gtc aag ggc tac cgc	624
Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg	
195 200 205	
gac gac ttc aag ccc gcc agc ggc gac ggc cag atc ggc atc gtc ctg	672
Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu	
210 215 220	
aac ggc gac ttc acc tac ccc tgg gac gcc gcc gac ccg gcc gac aag	720
Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys	
225 230 235 240	
gag gcg gcc gag cgg cgc ctg gag ttc ttc acg gcc tgg ttc gcg gac	768
Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp	
245 250 255	
ccc atc tac ttg ggc gac tac ccg gcg tcg atg cgc aag cag ctg ggc	816
Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly	
260 265 270	
gac ccg ctg ccg acc ttt acg ccc gag gag cgc gcc ctg gtc cac ggc	864
Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly	
275 280 285	
tcc aac gac ttt tac ggc atg aac cac tac acg tcc aac tac atc cgc	912
Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg	
290 295 300	
cac cgc agc tcg ccc gcc tcc gcc gac gac acc gtc ggc aac gtc gac	960
His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp	
305 310 315 320	
gtg ctg ttc acc aac aag cag ggc aac tgc atc ggc ccc gag acg cag	1008
Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln	
325 330 335	
tcc ccc tgg ctg cgc ccc tgt gcc gcc ggc ttc cgc gac ttc ctg gtg	1056
Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val	
340 345 350	
tgg atc agc aag agg tac ggc tac ccg ccc atc tac gtg acg gag aac	1104
Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn	
355 360 365	
ggc acg agc atc aag ggc gag agc gac ttg ccc aag gag aag att ctg	1152
Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu	
370 375 380	

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gaa gat gac ttc agg gtc aag tac tat aac gag tac atc cgt gcc atg      1200
Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
385                               390                               395                               400

gtt acc gcc gtg gag ctg gac ggg gtc aac gtc aag ggg tac ttt gcc      1248
Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
                               405                               410                               415

tgg tcg ctc atg gac aac ttt gag tgg gcg gac ggc tac gtg acg agg      1296
Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
                               420                               425                               430

ttt ggg gtt acg tat gtg gat tat gag aat ggg cag aag cgg ttc ccc      1344
Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
                               435                               440                               445

aag aag agc gca aag agc ttg aag ccg ctg ttt gac gag ctg att gcg      1392
Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
                               450                               455                               460

gcg gcg tga
Ala Ala
465

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<210> 90
<211> 466
<212> PRT
<213> Artificial Sequence

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<220>
<223> Synthetic Construct

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<400> 90

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Met Leu Pro Lys Asp Phe Gln Trp Gly Phe Ala Thr Ala Ala Tyr Gln
1                               5                               10                               15

Ile Glu Gly Ala Val Asp Gln Asp Gly Arg Gly Pro Ser Ile Trp Asp
                               20                               25                               30

Thr Phe Cys Ala Gln Pro Gly Lys Ile Ala Asp Gly Ser Ser Gly Val
                               35                               40                               45

Thr Ala Cys Asp Ser Tyr Asn Arg Thr Ala Glu Asp Ile Ala Leu Leu
                               50                               55                               60

Lys Ser Leu Gly Ala Lys Ser Tyr Arg Phe Ser Ile Ser Trp Ser Arg
65                               70                               75                               80

Ile Ile Pro Glu Gly Gly Arg Gly Asp Ala Val Asn Gln Ala Gly Ile
                               85                               90                               95

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Asp His Tyr Val Lys Phe Val Asp Asp Leu Leu Asp Ala Gly Ile Thr
 100 105 110
 Pro Phe Ile Thr Leu Phe His Trp Asp Leu Pro Glu Gly Leu His Gln
 115 120 125
 Arg Tyr Gly Gly Leu Leu Asn Arg Thr Glu Phe Pro Leu Asp Phe Glu
 130 135 140
 Asn Tyr Ala Arg Val Met Phe Arg Ala Leu Pro Lys Val Arg Asn Trp
 145 150 155 160
 Ile Thr Phe Asn Glu Pro Leu Cys Ser Ala Ile Pro Gly Tyr Gly Ser
 165 170 175
 Gly Thr Phe Ala Pro Gly Arg Gln Ser Thr Ser Glu Pro Trp Thr Val
 180 185 190
 Gly His Asn Ile Leu Val Ala His Gly Arg Ala Val Lys Ala Tyr Arg
 195 200 205
 Asp Asp Phe Lys Pro Ala Ser Gly Asp Gly Gln Ile Gly Ile Val Leu
 210 215 220
 Asn Gly Asp Phe Thr Tyr Pro Trp Asp Ala Ala Asp Pro Ala Asp Lys
 225 230 235 240
 Glu Ala Ala Glu Arg Arg Leu Glu Phe Phe Thr Ala Trp Phe Ala Asp
 245 250 255
 Pro Ile Tyr Leu Gly Asp Tyr Pro Ala Ser Met Arg Lys Gln Leu Gly
 260 265 270
 Asp Arg Leu Pro Thr Phe Thr Pro Glu Glu Arg Ala Leu Val His Gly
 275 280 285
 Ser Asn Asp Phe Tyr Gly Met Asn His Tyr Thr Ser Asn Tyr Ile Arg
 290 295 300
 His Arg Ser Ser Pro Ala Ser Ala Asp Asp Thr Val Gly Asn Val Asp
 305 310 315 320

Val Leu Phe Thr Asn Lys Gln Gly Asn Cys Ile Gly Pro Glu Thr Gln
 325 330 335

Ser Pro Trp Leu Arg Pro Cys Ala Ala Gly Phe Arg Asp Phe Leu Val
 340 345 350

Trp Ile Ser Lys Arg Tyr Gly Tyr Pro Pro Ile Tyr Val Thr Glu Asn
 355 360 365

Gly Thr Ser Ile Lys Gly Glu Ser Asp Leu Pro Lys Glu Lys Ile Leu
 370 375 380

Glu Asp Asp Phe Arg Val Lys Tyr Tyr Asn Glu Tyr Ile Arg Ala Met
 385 390 395 400

Val Thr Ala Val Glu Leu Asp Gly Val Asn Val Lys Gly Tyr Phe Ala
 405 410 415

Trp Ser Leu Met Asp Asn Phe Glu Trp Ala Asp Gly Tyr Val Thr Arg
 420 425 430

Phe Gly Val Thr Tyr Val Asp Tyr Glu Asn Gly Gln Lys Arg Phe Pro
 435 440 445

Lys Lys Ser Ala Lys Ser Leu Lys Pro Leu Phe Asp Glu Leu Ile Ala
 450 455 460

Ala Ala
 465

<210> 91
 <211> 2103
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Trichoderma reesei β -Glucosidase D

<220>
 <221> CDS
 <222> (1)..(2103)
 <223> Trichoderma reesei β -Glucosidase D

<400> 91
 atg att ctc ggc tgt gaa agc aca ggt gtc atc tct gcc gtc aaa cac
 Met Ile Leu Gly Cys Glu Ser Thr Gly Val Ile Ser Ala Val Lys His
 1 5 10 15

48

ttt gtc gcc aac gac cag gag cac gag cgg cga gcg gtc gac tgt ctc Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu 20 25 30	96
atc acc cag cgg gct ctc cgg gag gtc tat ctg cga ccc ttc cag atc Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile 35 40 45	144
gta gcc cga gat gca agg ccc ggc gca ttg atg aca tcc tac aac aag Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys 50 55 60	192
gtc aat ggc aag cac gtc gct gac agc gcc gag ttc ctt cag ggc att Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile 65 70 75 80	240
ctc cgg act gag tgg aat tgg gac cct ctc att gtc agc gac tgg tac Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr 85 90 95	288
ggc acc tac acc act att gat gcc atc aaa gcc ggc ctt gat ctc gag Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu 100 105 110	336
atg cgg gcc gtt tca cga tat cgc ggc aaa tac atc gag tct gct ctg Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu 115 120 125	384
cag gcc cgt ttg ctg aag cag tcc act atc gat gag cgc gct cgc cgc Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg 130 135 140	432
gtg ctc agg ttc gcc cag aag gcc agc cat ctc aag gtc tcc gag gta Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val 145 150 155 160	480
gag caa ggc cgt gac ttc cca gag gat cgc gtc ctc aac cgt cag atc Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile 165 170 175	528
tgc ggc agc agc att gtc cta ctg aag aat gag aac tcc atc tta cct Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro 180 185 190	576
ctc ccc aag tcc gtc aag aag gtc gcc ctt gtt ggt tcc cac gtg cgt Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg 195 200 205	624
cta ccg gct atc tcg gga gga ggc agc gcc tct ctt gtc cct tac tat Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr 210 215 220	672
gcc ata tct cta tac gat gcc gtc tct gag gta cta gcc ggt gcc acg Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr 225 230 235 240	720
atc acg cac gag gtc ggt gcc tat gcc cac caa atg ctg ccc gtc atc	768

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile	
245 250 255	
gac gca atg atc agc aac gcc gta atc cac ttc tac aac gac ccc atc	816
Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile	
260 265 270	
gat gtc aaa gac aga aag ctc ctt gcc agt gag aac gta tcg tcg aca	864
Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr	
275 280 285	
tcg ttc cag ctc atg gat tac aac aac atc cca acg ctc aac aag gcc	912
Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala	
290 295 300	
arg ttc tgg ggt act ctc gtg ggc gag ttt atc cct acc gcc acg gga	960
Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly	
305 310 315 320	
att tgg gaa ttt gcc ctc agt gtc ttt gcc act gcc gac ctt tat att	1008
Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile	
325 330 335	
gat aat gag ctc gtg att gaa aat aca aca cat cag acg cgt gga acc	1056
Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr	
340 345 350	
gcc ttt ttc gga aag gga acg acg gaa aaa gtc gct acc agg agg atg	1104
Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met	
355 360 365	
gtg gcc gcc agc acc tac aag ctg cgt ctc gag ttt ggg tct gcc aac	1152
Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn	
370 375 380	
acg acc aag atg gag acg acc ggt gtt gtc aac ttt gcc gcc ggt gcc	1200
Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala	
385 390 395 400	
gta cac ctg ggt gcc tgt ctc aag gtc gac cca cag gag atg att gcg	1248
Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala	
405 410 415	
cgg gcc gtc aag gcc gca gcc gat gcc gac tac acc atc atc tgc acg	1296
Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr	
420 425 430	
gga ctc agc gcc gag tgg gag tct gag ggt ttt gac cgg cct cac atg	1344
Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met	
435 440 445	
gac ctg ccc cct ggt gtg gac acc atg atc tcg caa gtt ctt gac gcc	1392
Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala	
450 455 460	
gct ccc aat gct gta gtc gtc aac cag tca gcc acc cca gtg aca atg	1440
Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met	
465 470 475 480	

agc tgg gct cat aaa gca aag gcc att gtg cag gct tgg tat ggt ggt Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly 485 490 495	1488
aac gag aca ggc cac gga atc tcc gat gtg ctc ttt ggc aac gtc aac Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn 500 505 510	1536
ccg tcg ggg aaa ctc tcc cta tcg tgg cca gtc gat gtg aag cac aac Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn 515 520 525	1584
cca gca tat ctc aac tac gcc agc gtt ggt gga cgg gtc ttg tat ggc Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly 530 535 540	1632
gag gat gtt tac gtt ggc tac aag ttc tac gac aaa acg gag agg gag Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu 545 550 555 560	1680
gtt ctg ttt cct ttt ggg cat gcc ctg tct tac gct acc ttc aag ctc Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu 565 570 575	1728
cca gat tct acc gtg agg acg gtc ccc gaa acc ttc cac ccg gac cag Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln 580 585 590	1776
ccc aca gta gcc att gtc aag atc aag aac acg agc agt gtc ccg ggc Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly 595 600 605	1824
gcc cag gtc ctg cag tta tac att tcg gcc cca aac tcg cct aca cat Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His 610 615 620	1872
cgc ccg gtc aag gag ctg cac gga ttc gaa aag gtg tat ctt gaa gct Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala 625 630 635 640	1920
ggc gag gag aag gag gta caa ata ccc att gac cag tac gct act agc Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser 645 650 655	1968
ttc tgg gac gag att gag agc atg tgg aag agc gag agg ggc att tat Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly Ile Tyr 660 665 670	2016
gat gtg ctt gta gga ttc tcg agt cag gaa atc tcg ggc aag ggg aag Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys 675 680 685	2064
ctg att gtg cct gaa acg cga ttc tgg atg ggg ctg tag Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu 690 695 700	2103

<210> 92
 <211> 700
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic Construct

<400> 92

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Phe Val Ala Asn Asp Gln Glu His Glu Arg Arg Ala Val Asp Cys Leu
 20 25 30

Ile Thr Gln Arg Ala Leu Arg Glu Val Tyr Leu Arg Pro Phe Gln Ile
 35 40 45

Val Ala Arg Asp Ala Arg Pro Gly Ala Leu Met Thr Ser Tyr Asn Lys
 50 55 60

Val Asn Gly Lys His Val Ala Asp Ser Ala Glu Phe Leu Gln Gly Ile
 65 70 75 80

Leu Arg Thr Glu Trp Asn Trp Asp Pro Leu Ile Val Ser Asp Trp Tyr
 85 90 95

Gly Thr Tyr Thr Thr Ile Asp Ala Ile Lys Ala Gly Leu Asp Leu Glu
 100 105 110

Met Pro Gly Val Ser Arg Tyr Arg Gly Lys Tyr Ile Glu Ser Ala Leu
 115 120 125

Gln Ala Arg Leu Leu Lys Gln Ser Thr Ile Asp Glu Arg Ala Arg Arg
 130 135 140

Val Leu Arg Phe Ala Gln Lys Ala Ser His Leu Lys Val Ser Glu Val
 145 150 155 160

Glu Gln Gly Arg Asp Phe Pro Glu Asp Arg Val Leu Asn Arg Gln Ile
 165 170 175

Cys Gly Ser Ser Ile Val Leu Leu Lys Asn Glu Asn Ser Ile Leu Pro
 180 185 190

Leu Pro Lys Ser Val Lys Lys Val Ala Leu Val Gly Ser His Val Arg
 195 200 205

Leu Pro Ala Ile Ser Gly Gly Gly Ser Ala Ser Leu Val Pro Tyr Tyr
 210 215 220

Ala Ile Ser Leu Tyr Asp Ala Val Ser Glu Val Leu Ala Gly Ala Thr
 225 230 235 240

Ile Thr His Glu Val Gly Ala Tyr Ala His Gln Met Leu Pro Val Ile
 245 250 255

Asp Ala Met Ile Ser Asn Ala Val Ile His Phe Tyr Asn Asp Pro Ile
 260 265 270

Asp Val Lys Asp Arg Lys Leu Leu Gly Ser Glu Asn Val Ser Ser Thr
 275 280 285

Ser Phe Gln Leu Met Asp Tyr Asn Asn Ile Pro Thr Leu Asn Lys Ala
 290 295 300

Met Phe Trp Gly Thr Leu Val Gly Glu Phe Ile Pro Thr Ala Thr Gly
 305 310 315 320

Ile Trp Glu Phe Gly Leu Ser Val Phe Gly Thr Ala Asp Leu Tyr Ile
 325 330 335

Asp Asn Glu Leu Val Ile Glu Asn Thr Thr His Gln Thr Arg Gly Thr
 340 345 350

Ala Phe Phe Gly Lys Gly Thr Thr Glu Lys Val Ala Thr Arg Arg Met
 355 360 365

Val Ala Gly Ser Thr Tyr Lys Leu Arg Leu Glu Phe Gly Ser Ala Asn
 370 375 380

Thr Thr Lys Met Glu Thr Thr Gly Val Val Asn Phe Gly Gly Gly Ala
 385 390 395 400

Val His Leu Gly Ala Cys Leu Lys Val Asp Pro Gln Glu Met Ile Ala
 405 410 415

Arg Ala Val Lys Ala Ala Ala Asp Ala Asp Tyr Thr Ile Ile Cys Thr
 420 425 430

Gly Leu Ser Gly Glu Trp Glu Ser Glu Gly Phe Asp Arg Pro His Met
 435 440 445
 Asp Leu Pro Pro Gly Val Asp Thr Met Ile Ser Gln Val Leu Asp Ala
 450 455 460
 Ala Pro Asn Ala Val Val Val Asn Gln Ser Gly Thr Pro Val Thr Met
 465 470 475 480
 Ser Trp Ala His Lys Ala Lys Ala Ile Val Gln Ala Trp Tyr Gly Gly
 485 490 495
 Asn Glu Thr Gly His Gly Ile Ser Asp Val Leu Phe Gly Asn Val Asn
 500 505 510
 Pro Ser Gly Lys Leu Ser Leu Ser Trp Pro Val Asp Val Lys His Asn
 515 520 525
 Pro Ala Tyr Leu Asn Tyr Ala Ser Val Gly Gly Arg Val Leu Tyr Gly
 530 535 540
 Glu Asp Val Tyr Val Gly Tyr Lys Phe Tyr Asp Lys Thr Glu Arg Glu
 545 550 555 560
 Val Leu Phe Pro Phe Gly His Gly Leu Ser Tyr Ala Thr Phe Lys Leu
 565 570 575
 Pro Asp Ser Thr Val Arg Thr Val Pro Glu Thr Phe His Pro Asp Gln
 580 585 590
 Pro Thr Val Ala Ile Val Lys Ile Lys Asn Thr Ser Ser Val Pro Gly
 595 600 605
 Ala Gln Val Leu Gln Leu Tyr Ile Ser Ala Pro Asn Ser Pro Thr His
 610 615 620
 Arg Pro Val Lys Glu Leu His Gly Phe Glu Lys Val Tyr Leu Glu Ala
 625 630 635 640
 Gly Glu Glu Lys Glu Val Gln Ile Pro Ile Asp Gln Tyr Ala Thr Ser
 645 650 655

Phe Trp Asp Glu Ile Glu Ser Met Trp Lys Ser Glu Arg Gly-Ile Tyr
 660 665 670

Asp Val Leu Val Gly Phe Ser Ser Gln Glu Ile Ser Gly Lys Gly Lys
 675 680 685

Leu Ile Val Pro Glu Thr Arg Phe Trp Met Gly Leu
 690 695 700

<210> 93
 <211> 1496
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHI

<400> 93
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 ggacccacgc caccacctcc tccaccaact gctacgacgg caacacctgg tctccaccc 180
 tctgcccgga caacgagacc tgcgccaaga actgtgcct cgacggcgcc gcctacgcct 240
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 cccagaagaa cgtggcgcc cgctctacc tcatggcctc cgacaccacc taccaggagt 360
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 tcaacggcgc cctctacttc gtgtccatgg acgccgacgg cggcgtgtcc aagtaccgga 480
 ccaacaccgc cggcgccaag tacggcaccg gctactgcga ctcccagtc ccgcgcgacc 540
 tcaagtccat caacggccag gccaacgtgg agggctggga gccgtcctcc aacaacgcca 600
 acaccggcat cggcggccac ggctcctgct gctccgagat ggacatctgg gaggccaaact 660
 ccatctccga ggccctcacc ccgcaccctg gcaccaccgt gggccaggag atctgcgagg 720
 gcgacggctg cggcggcacc tactccgaca accgctacgg cggcacctgc gacccggacg 780
 gctgcgactg gaacccttac cgctcggca acacctcct ctacggcccg ggctcctcct 840
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 gcccgaccca gtcccactac ggccagtgcg gcggcatcgg ctactccggc ccgaccgtgt 1440
 gcgcctccgg caccacctgc cagggtgctca acccgctacta ctcccagtgc ctctag 1496

<210> 94
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CBHII

<400> 94
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 aactggctcg gcccgacctg ctgcgcctcc ggctccacct gcgtgtactc caacgactac 120
 tactccagtc gcctcccggt cgcgcctcc tcctcctcct ccacccgcg cgcctccacc 180
 acctcccgcg tgctcccgac cactcccgcc tcctcctccg ccacccgcc gccgggctcc 240
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 ccgtccctca ccggcgccat ggccaccgccc gccgcgcggc tggccaaggc gccgtcttc 420
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 accgccaaca agaacggcgg caactacgcc ggccagtctg tgggttacga cctcccgac 540
 cgcgactcgc ccgcccctgc ctccaacggc gagtactcca tcgccgacgg cggcgtggcc 600
 aagtacaaga actacatcga caccatccgc cagatcgtgg tggagtactc cgacatccgc 660
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 aacctccgga acgtggccat gtacctcgac gccggccacg ccggctggct cggctggccg 840
 gccaaaccag acccgccgcg ccagctcttc gccaacgtgt acaagaacgc ctctccccc 900
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tccggcaagc agccgaccgg ccagcagcag tggggcgact ggtgcaacgt gatcggcacc 1140
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gtgaagccgg gcggcgagtg cgacggcacc tccgactcct ccgccccgcg cttcgactcc 1260
cactgcgccc tcccggacgc cctccagccg gccccgcagg ccggcgcttg gttccaggcc 1320
tacttcgtgc agtcctcac caacgccaac ccgtccttcc tctag 1365

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<210> 95
<211> 1317
<212> DNA
<213> Artificial Sequence

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<220>
<223> Maize optimized EGLI

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<400> 95
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tgatgcacg acgccaacta caactcctgc accgtgaacg gcggcgtaga caccaccctc 180
tggccggacg aggccacctg cggcaagaac tgcttcatcg agggcgtaga ctacgccgcc 240
tccggcgtag ccacctccgg ctctcctc accatgaacc agtacatgcc gtctcctcc 300
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tccaccgagg gcaaccgctc caacaccctc gccaaacaacc cgaacacca cgtgggtgtc 1080
tccaacatcc gctggggcga catcgggtcc accaccaact ccaccgccc gccgcccgcg 1140

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cgggctctct ccaccacctt ctccaccacc cgccgctcct ccaccacctc ctctctcccc 1200
 tcttgcaccc agaccacttg gggccagtgc ggcggcatcg gctactccgg ctgcaagacc 1260
 tgcacctccg gcaccacctg ccagtactcc aacgactact actcccagtg cctctag 1317

<210> 96
 <211> 1401
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized BGLII

<400> 96
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 gtggaccagg acggccgcgg ccggtccatc tgggacacct tctgcgcca gccgggcaag 120
 atcgccgacg gctcctccgg cgtgaccgcc tgcgactcct acaaccgcac cgccgaggac 180
 atcgccctcc tcaagtccct cggcgccaag tctaccgct tctccatctc ctgggtccgc 240
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gacaacttcg agtgggcccga cggctacgtg acccgcttcg gcgtgacctg cgtggactac 1320
 gagaacggcc agaagcgctt cccgaagaag tccgccaagt ccctcaagcc gctcttcgac 1380
 gagctcatcg ccgccccta g 1401

<210> 97
 <211> 2103
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Maize optimized CEL3D

<400> 97
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 gtgtacctcc gcccggtcca gatcgtggcc cgcgacgccc gcccgggcg cctcatgacc 180
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 tag 2103

<210> 98
 <211> 420
 <212> DNA
 <213> Zea mays

<220>
 <223> Q protein promoter

<400> 98
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 acaagtaaca caatattaca aagttagttt catacaaagc aagaaaagga caataatact 180
 tgacatgtaa agtgaagctt attatacttc ctaatccaac acaaaacaaa aaaaagttgc 240
 acaaaaggtcc aaaaatccac atcaaccatt aacctatacg taaagtgagt gatgagtcac 300
 atratccaac aaatgtttat caatgtggta tcatacaagc attgacatcc cataaatgca 360
 agaaattgtg ccaacaaagc tataagtaac cctcatatgt atttgactc atgcatcaca 420

<210> 99
 <211> 1188

<212> DNA
 <213> artificial sequence

<220>
 <223> synthetic ferulic acid esterase

<400> 99
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 ccgcgcggcc aggtggtgaa catctcctac ttctccaccg ccaccaactc caccgcgccg 120
 gcccgcgtgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
 ctccacggca tcggcggctc cgagaacgac tggttcgagg gcggcggccg cgccaacgtg 240
 atcgccgaca acctcatcgc cgagggcaag atcaagccgc tcatcatcgt gaccccgaac 300
 accaacgcgc ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctcctc 360
 aactccctca tcccgtaaat cgagtcgaac tactccgtgt acaccgaccg cgagcaccgc 420
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 aacatcaacc acgtgtactg gctcatccag ggccggcggc acgacttcaa cgtgtggaag 720
 ccgggcctct ggaacttctt ccagatggc gacgaggccg gcctcaccgc cgacggcaac 780
 accccggtgc cgaccccgtc ccgaagccg gccaacaccc gcatcgaggc cgaggactac 840
 gacggcatca actcctctc catcgagatc atcggcgtgc cgcgggaggg cggccgcggc 900
 atcggctaca tcacctcgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960
 gccacctctt tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgcctc 1020
 aacggcccga acggcaccct catcggcacc ctctccgtga agtccaccgg cgactggaac 1080
 acctacgagg agcagacctg ctccatctcc aaggtgaccg gcatcaacga cctctacctc 1140
 gtgttcaagg gcccggtgaa catcgactgg ttacacctcg gcgtgtag 1188

<210> 100
 <211> 395
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic ferulic acid esterase

<400> 100

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
 1 5 10 15
 Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
 20 25 30
 Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
 35 40 45
 Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
 50 55 60
 Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
 65 70 75 80
 Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
 85 90 95
 Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
 100 105 110
 Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
 115 120 125
 Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
 130 135 140
 Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
 145 150 155 160
 Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
 165 170 175
 Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
 180 185 190
 Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
 195 200 205
 Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
 210 215 220
 Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
 225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
 245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
 260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
 275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
 290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
 305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
 325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
 340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
 355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
 370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 385 390 395

<210> 101
 <211> 1188
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13036

<400> 101
 atggccgct cctcccgac catgccgcg tccggctacg accaggtgcg caacggcgtg 60
 ccgcgcggcc aggtggtgaa catctctac ttctccaccg ccaccaactc caccgcccg 120
 gcccgctgt acctcccgcc gggctactcc aaggacaaga agtactccgt gctctacctc 180
 ctccacgga tcggcggctc cgagaacgac tggttcgagg gcggcgccg cgccaacgtg 240

```

atcgccgaca acctcatcgc cgagggaag atcaagccgc tcatcatcgt gaccccgaaac 300
accaacgccc ccggcccggg catcgccgac ggctacgaga acttcaccaa ggacctcctc 360
aactccctca tcccgatcat cgagtcacaac tactccgtgt acaccgaccg cgagcaccgc 420
gccatcgccg gcctctctat gggcgccggc cagtccttca acatcggcct caccaacctc 480
gacaagtctg cctacatcgg ccgatctcc gccgcccga acacctacc gaacgagcgc 540
ctcttcccgg acggcggaac ggccgccgc gagaagctca agctcctctt catcgctgc 600
ggcaccacg actccctcat cggttcggc cagcgctgc acgagtactg cgtggccaac 660
aacatcaacc acgtgtactg gctcatccag ggcggcgcc acgacttcaa cgtgtggaag 720
ccgggctctt ggaacttctt ccgatggcc gacgaggccg gcctcaccg cgacggcaac 780
accccggtgc cgaccccgtc ccgaagccg gccaacacc gcacgaggc cgaggactac 840
gacggcatac actcctctc catcgagatc atcggcgtgc cgccggaggg cggccgcggc 900
atcggtaca tcacctcgg cgactacctc gtgtacaagt ccatcgactt cggcaacggc 960
gccacctctt tcaaggccaa ggtggccaac gccaacacct ccaacatcga gcttcgctc 1020
aacggcccga acggcacctt catcggcacc ctctccgtga agtccaccg cgactggaac 1080
acctacgagg agcagacctg ctccatctcc aaggtagccg gcatcaacga cctctacctc 1140
gtgttcaagg gcccggtgaa catcgactgg ttacacctcg gcgtgtag 1188

```

```

<210> 102
<211> 395
<212> PRT
<213> artificial sequence

```

```

<220>
<223> plasmid 13036

```

```

<400> 102

```

```

Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val
1           5           10           15

```

```

Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser
20           25           30

```

```

Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro Gly
35           40           45

```

```

Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile
50           55           60

```

Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val
65 70 75 80

Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile
85 90 95

Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr
100 105 110

Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu
115 120 125

Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly
130 135 140

Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu
145 150 155 160

Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr
165 170 175

Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys
180 185 190

Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly
195 200 205

Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His
210 215 220

Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys
225 230 235 240

Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr
245 250 255

Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn
260 265 270

Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile
275 280 285

Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile
290 295 300

Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly
305 310 315 320

Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile
325 330 335

Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser
340 345 350

Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser
355 360 365

Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly
370 375 380

Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
385 390 395

<210> 103
<211> 1245
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 13038

<400> 103
atgagggtgt tgctcgttgc cctcgtcttc ctggctctcg ctgcgagcgc cacctccatg 60
gccgcctccc tcccgaacct gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
cgcgccagg tggagaacat ctctacttc tccaccgcca ccaactccac ccgcccggcc 180
cgcggtgtacc tcccgcgggg ctactccaag gacaagaagt actccgtgct ctacctctc 240
cacggcatcg gcggctcga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac cccgaacacc 360
aacgccgccg gcccgggcat cgccgacggc tacgagaact tcaccaagga cctctcaac 420
tccctcatcc cgtacatcga gtccaaactac tccgtgtaca ccgaccgca gcaccgcgcc 480
atcgccggcc tctctatggg cggcgggcag tcttcaaca tcggcctcac caacctcgac 540
aagttcgct acatcgggcc gatctccgcc gccccgaaca cctacccgaa cgagcgctc 600
ttccggagc gcggcaaggc cggccgcgag aagctcaagc tctcttcat cgcctgcggc 660


```

accaaagact ccctcatcgg cttcggccag cgcgtgcacg agtactgcgt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
ggcctctgga acttctcca gatggccgac gaggcgggcc tcacccgcga cggcaacacc 840
ccggtgcccga ccccgctccc gaagccggcc aacaccgcga tcgaggccga ggactacgac 900
ggcatcaact cctcctccat cgagatcatc ggcgtgcgcg cggagggcgg ccgcggcctc 960
ggctacatca cctcgggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
ggcccgaacg gcacctcat cggcacctc tccgtgaagt ccaccggcga ctggaacacc 1140
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
ttcaagggcc cggagaacat cgactgggtc accttcggcg tgtag 1245

```

```

<210> 104
<211> 414
<212> PRT
<213> artificial sequence

```

```

<220>
<223> plasmid 13038 aa

```

```

<400> 104

```

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20           25           30

```

```

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35           40           45

```

```

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50           55           60

```

```

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65           70           75           80

```

```

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
85           90           95

```

```

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
100          105          110

```

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125
 Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140
 Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160
 Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175
 Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190
 Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205
 Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220
 Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240
 Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255
 Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270
 Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285
 Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300
 Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
 305 310 315 320
 Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
 325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
 340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
 355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
 370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
 385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 405 410

<210> 105
 <211> 1425
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13039

<400> 105
 atgctgqcg cgtctggccac gtcgcagctc gtcgcaacgc gcgccggcct gggcgctccc 60
 gacgcgtcca cgttcgcgcg cggcgccgcg cagggcctga ggggggccc ggcgtcggcg 120
 gcggcggaaca cgtcagcat gcggaccagc gcgcgcgcgg cggccaggca ccagcaccag 180
 caggcgcgcc gcggggccag gttcccgctc ctcgtcgtgt gcgccagcgc cggcgccatg 240
 gccgcctccc tcccgaccat gccgcgcgtc ggctacgacc aggtgcgcaa cggcggtgcc 300
 cggcgccagg tggatgaacat ctctacttc tccaccgcca ccaactccac ccgcccgcc 360
 cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctctc 420
 cacggcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 480
 gccgacaacc tcatcgccga gggcaagatc aagccgctca tcatcgtgac ccggaacacc 540
 aacgcgcgcg gcccgggcat cgcgcgagc tacgagaact tcaccaagga cctcctcaac 600
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 660
 atcgccggcc tctctatggg cggcggccag tccttcaaca tcggcctcac caacctcgac 720
 aagttcgctt acatcgccc gatctcgcc gccccgaaca cctaccgaa cgagcgctc 780
 tccccgagc gcggcaaggc cggcgcgag aagctcaagc tcctcttcat cgctgcggc 840
 accaacgact cctcatcg cttcggccag cgcgtgcacg agtactgct ggccaacaac 900

```

atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg    960
ggcctctgga acttctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc    1020
ccggcgccga ccccgcccc gaagccggcc aacaccgcga tcgaggccga ggactacgac    1080
ggcatcaact cctcctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc    1140
ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc    1200
acctccttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac    1260
ggcccgaacg gcacctcat cggcacctc tccgtgaagt ccaccggcga ctggaacacc    1320
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg    1380
ttcaagggcc cggagaacat cgactggttc accttcggcg tgtag                    1425

```

<210> 106
 <211> 474
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13039 aa

<400> 106

```

Met Leu Ala Ala Leu Ala Thr Ser Gln Leu Val Ala Thr Arg Ala Gly
1           5           10           15

```

```

Leu Gly Val Pro Asp Ala Ser Thr Phe Arg Arg Gly Ala Ala Gln Gly
          20           25           30

```

```

Leu Arg Gly Ala Arg Ala Ser Ala Ala Ala Asp Thr Leu Ser Met Arg
          35           40           45

```

```

Thr Ser Ala Arg Ala Ala Pro Arg His Gln His Gln Gln Ala Arg Arg
          50           55           60

```

```

Gly Ala Arg Phe Pro Ser Leu Val Val Cys Ala Ser Ala Gly Ala Met
65           70           75           80

```

```

Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr Asp Gln Val Arg
          85           90           95

```

```

Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser Tyr Phe Ser Thr
          100          105          110

```

Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu Pro Pro-Gly Tyr
 115 120 125
 Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu His Gly Ile Gly
 130 135 140
 Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg Ala Asn Val Ile
 145 150 155 160
 Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro Leu Ile Ile Val
 165 170 175
 Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala Asp Gly Tyr Glu
 180 185 190
 Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro Tyr Ile Glu Ser
 195 200 205
 Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala Ile Ala Gly Leu
 210 215 220
 Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu Thr Asn Leu Asp
 225 230 235 240
 Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro Asn Thr Tyr Pro
 245 250 255
 Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala Arg Glu Lys Leu
 260 265 270
 Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser Leu Ile Gly Phe
 275 280 285
 Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn Ile Asn His Val
 290 295 300
 Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn Val Trp Lys Pro
 305 310 315 320
 Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala Gly Leu Thr Arg
 325 330 335
 Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys Pro Ala Asn Thr
 340 345 350

Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser Ser Ser Ile Glu
 355 360 365

Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile Gly Tyr Ile Thr
 370 375 380

Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe Gly Asn Gly Ala
 385 390 395 400

Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr Ser Asn Ile Glu
 405 410 415

Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly Thr Leu Ser Val
 420 425 430

Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln Thr Cys Ser Ile
 435 440 445

Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val Phe Lys Gly Pro
 450 455 460

Val Asn Ile Asp Trp Phe Thr Phe Gly Val
 465 470

<210> 107
 <211> 1263
 <212> DNA
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 107
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 gccgcctccc tcccgaccat gccgccgtcc ggctacgacc aggtgcgcaa cggcgtgccg 120
 cgcggccagg tgggtgaacat ctctacttcc tccaccgcca ccaactccac ccgcccggcc 180
 cgcgtgtacc tcccgccggg ctactccaag gacaagaagt actccgtgct ctacctcttc 240
 caccgcatcg gcggctccga gaacgactgg ttcgagggcg gcggccgcgc caacgtgatc 300
 gccgacaacc tcctcggcga gggcaagatc aagccgctca tcctcgtgac cccgaacacc 360
 aacgccgcgc gcccgggcat cgcgcagcgc tacgagaact tcaccaagga cctcctcaac 420
 tccctcatcc cgtacatcga gtccaactac tccgtgtaca ccgaccgcga gcaccgcgcc 480

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atcgccggcc tctctatggg cggcggccag tcttcaaca tcggcctcac caacctcgac 540
aagttcgctt acatcgggcc gatctccgcc gccccgaaca cctaccgaa cgagcgctc 600
ttcccggacg gcggcaaggc cggccgcgag aagctcaagc tctcttcat cgcctgcggc 660
accaacgact cctcatcgg cttcgggccag cgcgtgcacg agtactgctt ggccaacaac 720
atcaaccacg tgtactggct catccagggc ggcggccacg acttcaacgt gtggaagccg 780
ggcctctgga acttctcca gatggccgac gaggccggcc tcaccgcga cggcaacacc 840
ccggtgcga cccgtcccc gaagccggcc aacaccgca tcgaggccga ggactacgac 900
ggcatcaact cctctccat cgagatcatc ggcgtgccgc cggagggcgg ccgcggcatc 960
ggctacatca cctccggcga ctacctcgtg tacaagtcca tcgacttcgg caacggcgcc 1020
acctcttca aggccaaggt ggccaacgcc aacacctcca acatcgagct tcgcctcaac 1080
ggcccgaacg gcacctcat cggcaccctc tccgtgaagt ccaccggcga ctggaacacc 1140
tacgaggagc agacctgctc catctccaag gtgaccggca tcaacgacct ctacctcgtg 1200
ttcaagggcc cggtgaacat cgactggttc accttcggcg tgtccgagaa ggacgaactc 1260
tag 1263

```

<210> 108
 <211> 420
 <212> PRT
 <213> artificial sequence

<220>
 <223> plasmid 13347

<400> 108

```

Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Met Ala Ala Ser Leu Pro Thr Met Pro Pro Ser Gly Tyr
20           25           30

```

```

Asp Gln Val Arg Asn Gly Val Pro Arg Gly Gln Val Val Asn Ile Ser
35           40           45

```

```

Tyr Phe Ser Thr Ala Thr Asn Ser Thr Arg Pro Ala Arg Val Tyr Leu
50           55           60

```

```

Pro Pro Gly Tyr Ser Lys Asp Lys Lys Tyr Ser Val Leu Tyr Leu Leu
65           70           75           80

```

His Gly Ile Gly Gly Ser Glu Asn Asp Trp Phe Glu Gly Gly Gly Arg
 85 90 95

Ala Asn Val Ile Ala Asp Asn Leu Ile Ala Glu Gly Lys Ile Lys Pro
 100 105 110

Leu Ile Ile Val Thr Pro Asn Thr Asn Ala Ala Gly Pro Gly Ile Ala
 115 120 125

Asp Gly Tyr Glu Asn Phe Thr Lys Asp Leu Leu Asn Ser Leu Ile Pro
 130 135 140

Tyr Ile Glu Ser Asn Tyr Ser Val Tyr Thr Asp Arg Glu His Arg Ala
 145 150 155 160

Ile Ala Gly Leu Ser Met Gly Gly Gly Gln Ser Phe Asn Ile Gly Leu
 165 170 175

Thr Asn Leu Asp Lys Phe Ala Tyr Ile Gly Pro Ile Ser Ala Ala Pro
 180 185 190

Asn Thr Tyr Pro Asn Glu Arg Leu Phe Pro Asp Gly Gly Lys Ala Ala
 195 200 205

Arg Glu Lys Leu Lys Leu Leu Phe Ile Ala Cys Gly Thr Asn Asp Ser
 210 215 220

Leu Ile Gly Phe Gly Gln Arg Val His Glu Tyr Cys Val Ala Asn Asn
 225 230 235 240

Ile Asn His Val Tyr Trp Leu Ile Gln Gly Gly Gly His Asp Phe Asn
 245 250 255

Val Trp Lys Pro Gly Leu Trp Asn Phe Leu Gln Met Ala Asp Glu Ala
 260 265 270

Gly Leu Thr Arg Asp Gly Asn Thr Pro Val Pro Thr Pro Ser Pro Lys
 275 280 285

Pro Ala Asn Thr Arg Ile Glu Ala Glu Asp Tyr Asp Gly Ile Asn Ser
 290 295 300

Ser Ser Ile Glu Ile Ile Gly Val Pro Pro Glu Gly Gly Arg Gly Ile
305 310 315 320

Gly Tyr Ile Thr Ser Gly Asp Tyr Leu Val Tyr Lys Ser Ile Asp Phe
325 330 335

Gly Asn Gly Ala Thr Ser Phe Lys Ala Lys Val Ala Asn Ala Asn Thr
340 345 350

Ser Asn Ile Glu Leu Arg Leu Asn Gly Pro Asn Gly Thr Leu Ile Gly
355 360 365

Thr Leu Ser Val Lys Ser Thr Gly Asp Trp Asn Thr Tyr Glu Glu Gln
370 375 380

Thr Cys Ser Ile Ser Lys Val Thr Gly Ile Asn Asp Leu Tyr Leu Val
385 390 395 400

Phe Lys Gly Pro Val Asn Ile Asp Trp Phe Thr Phe Gly Val Ser Glu
405 410 415

Lys Asp Glu Leu
420

<210> 109
<211> 1296
<212> DNA
<213> artificial sequence

<220>
<223> plasmid 11267

<400> 109
atgagggtgt tgctcggtgc cctcgctctc ctggctctcg ctgcgagcgc caccagcgct 60
gcgcagtcgc agccggagct gaagctggag tccgtggtga tcgtgtcccg ccacggcggtg 120
cgcgccccga ccaaggccac ccagctcatg caggacgtga ccccgagcgc ctggccgacc 180
tggcgggtga agctcggcga gctgaccccg cgcggcgggc agctgatcgc ctacctcggc 240
cactactggc gccagcgctt cgtggccgac ggctcctcc cgaagtgcgg ctgcccgcag 300
tccggccagg tggccatcat cggcgacgtg gacgagcgca cccgcaagac cggcgaggcc 360
ttcgccggcg gctcgcgcc ggactgcgcc atcaccgtgc acaccaggc cgacacctcc 420
tccccggacc cgtcttcaa cccgctcaag accggcgtgt gccagctcga caacgccaac 480
gtgaccgacg ccattcctga gcgcgcggc ggctccatcg ccgacttcac cggccactac 540

```

cagaccgcct tccgcgagct ggagcgctg ctcaacttcc cgcagtcctc cctctgcctc 600
aagcgcgaga agcaggacga gtctgtctcc ctacccagg ccctcccgtc cgagctgaag 660
gtgtccgcgc actgcgtgtc cctcaccggc gccgtgtccc tcgcctccat gctcaccgaa 720
atcttctctcc tccaacaggc ccagggcctg ccggagccgg gctggggccg catcaccgac 780
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gccggctgag aggagcgcaa cgcacgggc atgtgtctcc tcgccggctt caccagatc 1260
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<223> plasmid 11267 aa sequence

<400> 110

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
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```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20           25           30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35           40           45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50           55           60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65           70           75           80

```

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Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
 325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
 340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
 355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
 370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
 385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
 405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
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 gtgaccgacg ccactctgga gcgcgcggc ggctccatcg ccgacttcac cggccactac 540
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atcttctctcc tccagcagga ccaggggcatg ccggagccgg gctggggccg catcaccgac    780
tcccaccagt ggaacacctt cctctccctc cacaacgccc agttcgacct cctccagcgc    840
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accccgcacc cggcgagaa gcaggcctac ggcgtgaccc tcccgacctc cgtgctcttc    960
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atgcgcgaca agaccccgct ctccctcaac acccgccgg gcgaggtgaa gctcaccctc   1200
gccggctgcg aggagcgcaa cggccagggc atgtgtctcc tcgccggctt caccagatc   1260
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<213> artificial sequence

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<223> plasmid 11268 amino acid sequence

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Met Arg Val Leu Leu Val Ala Leu Ala Leu Leu Ala Leu Ala Ala Ser
1           5           10           15

```

```

Ala Thr Ser Ala Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val
20           25           30

```

```

Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln
35           40           45

```

```

Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys
50           55           60

```

```

Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly
65           70           75           80

```

```

His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys Cys
85           90           95

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Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu
 100 105 110

Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp
 115 120 125

Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp Pro
 130 135 140

Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala Asn
 145 150 155 160

Val Thr Asp Ala Ile Leu Glu Arg Ala Gly Gly Ser Ile Ala Asp Phe
 165 170 175

Thr Gly His Tyr Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu Asn
 180 185 190

Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu Ser
 195 200 205

Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala Asp
 210 215 220

Cys Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr Glu
 225 230 235 240

Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp Gly
 245 250 255

Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His Asn
 260 265 270

Ala Gln Phe Asp Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser Arg
 275 280 285

Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His Pro
 290 295 300

Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu Phe
 305 310 315 320

Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu Glu
325 330 335

Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly Gly
340 345 350

Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln Trp
355 360 365

Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp Lys
370 375 380

Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr Leu
385 390 395 400

Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala Gly
405 410 415

Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu Ser
420 425 430

Glu Lys Asp Glu Leu
435